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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.005 Å R factor = 0.047 wR factor = 0.131 Data-to-parameter ratio = 8.2

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L-Methioninium nitrate

The asymmetric unit of the title compound, C_5H_{12} - $NO_2S^+ \cdot NO_3^-$, is composed of two crystallographically independent methioninium cations related by pseudosymmetry $(-x, \frac{1}{5} + y, \frac{1}{2} - z)$ and two nitrate anions related by a pseudoinversion centre at (0.50, 0.43, 0.25). In one of the residues, the straight side-chain conformation is *gauche* II–*trans–gauche* II, while in the other it is *gauche* II–*trans–trans*. In the crystal, the methioninium residues form N–H···O hydrogen-bonded molecular columns, which are interlinked by N–H···O and O–H···O hydrogen bonds involving the O atoms of the nitrate groups.

Comment

L-Methionine is one of the sulfur-containing amino acids. Apart from its role as a protein constituent and as an essential amino acid, methionine is also important as a donor of an active methyl group. The crystal structures of L-methionine (Torii & Iitaka, 1973), DL-methionine (α -form; Mathieson, 1952; Taniguchi *et al.*, 1980), L-methionine hydrochloride (Di Blasio *et al.*, 1977), DL-methionine nitrate (Mostad & Natarajan, 1985), bis(DL-methionine) dihydrogenphosphate (Asath Bahadur, 1992), bis(L-methioninium) sulfate (Srinivasan *et al.*, 2001) and L-methionine L-methioninium perchlorate (Sridhar *et al.*, 2002) have been reported. The present study of L-methionine reacted with nitric acid, (I), was undertaken to study the conformation and hydrogen-bonding pattern resulting from the presence of an inorganic acid.

$$2 \begin{bmatrix} COOH \\ I \\ H-C-CH_2-CH_2-S-CH_3 \\ I \\ NH_3^+ \end{bmatrix} \cdot (2NO_3)^{-1}$$

The asymmetric unit of (I) contains two crystallographically independent methioninium residues, 1 and 2, which are in the cationic form, and two nitrate anions (Fig. 1). The methioninium residues with their centroid at (0.50, 0.95, 0.25) are related by pseudosymmetry ($-x, \frac{1}{5} + y, \frac{1}{2} - z$). The deviation from this pseudosymmetry is large for atoms S21 and C25, as also evidenced from the different χ^3 angles. The two nitrate anions are related by a pseudo-inversion centre at (0.50, 0.43, 0.25).

The back-bone conformation angles ψ^1 for residues 1 and 2 are -27.6 (5) and -31.6 (5)°, respectively. Least-squares-

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© 2002 International Union of Crystallography Printed in Great Britain – all rights reserved plane calculations reveal that the deviations of the amino N atoms from the carboxyl groups are 0.64 (6) and 0.68 (6) Å for residues 1 and 2, respectively. This tendency for the C-Nbond to twist is found in various amino acids (Lakshminarayanan et al., 1967). All three possible rotational isomers are found to exist in the methioninium residues. In both the residues, the straight side-chain conformation angles χ^1 are in the gauche II form $[-72.4 (5) \text{ and } -66.6 (5)^{\circ}]$, while χ^2 are in the *trans* form $[-178.3 (3) \text{ and } -178.5 (3)^{\circ}]$. However, angle χ^3 adopts a gauche II form $[-85.7 (4)^\circ]$ in residue 1 and a *trans* form $[176.0 (3)^{\circ}]$ in residue 2.

Both the methioninium residues have similar hydrogenbonding features. The screw-related residues 1 are linked by N11-H11C···O1A(1-x, y-1/2, 1-z) hydrogen bonds to form a column-like structure around the 21 screw axis. Similarly, the screw-related residues 2 also form an independent molecular column around the 2_1 screw axis, through N21- $H21C \cdots O2A(1-x, y-1/2, -z)$ hydrogen bonds (Table 2). In the crystal, the molecular columns, formed independently by residues 1 and 2, are assembled alternately along the c-cell direction, and are interlinked by N-H···O and O-H···O hydrogen bonds involving the O atoms of the nitrate groups. The hydrophilic and hydrophobic groups are aggregated in two distinct regions in the crystal (Fig. 2).



Figure 2

Packing of the molecules, viewed down the b axis.

Crystal data

$C_5H_{12}NO_2S^+ \cdot NO_3^-$	D_m measured by flotation method in
$M_r = 212.23$	a mixture of carbon tetrachloride
Monoclinic, P2 ₁	and xylene
a = 10.682 (2) Å	Mo $K\alpha$ radiation
b = 5.577 (2) Å	Cell parameters from 25
c = 16.829 (6) Å	reflections
$\beta = 100.92 \ (2)^{\circ}$	$\theta = 2.1 - 24.9^{\circ}$
$V = 984.3 (5) \text{ Å}^3$	$\mu = 0.33 \text{ mm}^{-1}$
Z = 4	T = 293 (2) K
$D_x = 1.432 \text{ Mg m}^{-3}$	Plate, colourless
$D_m = 1.43 \text{ Mg m}^{-3}$	$0.5 \times 0.3 \times 0.2 \text{ mm}$

Data collection

Enraf-Nonis sealed-tube	$R_{\rm int} = 0.038$
diffractometer	$\theta_{\rm max} = 24.9^{\circ}$
ω –2 θ scans	$h = 0 \rightarrow 12$
Absorption correction: ψ scan	$k = 0 \rightarrow 6$
(North et al., 1968)	$l = -19 \rightarrow 19$
$T_{\min} = 0.892, \ T_{\max} = 0.937$	3 standard reflections
2028 measured reflections	frequency: 60 min
1924 independent reflections	intensity decay: none
1671 reflections with $I > 2\sigma(I)$	

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.0999P)^2]$ $R[F^2 > 2\sigma(F^2)] = 0.047$ where $P = (F_o^2 + 2F_c^2)/3$ $wR(F^2) = 0.131$ S = 1.04 $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.62 \text{ e } \text{\AA}^{-3}$ 1924 reflections $\Delta \rho_{\rm min} = -0.36 \text{ e } \text{\AA}^{-3}$ 235 parameters H-atom parameters constrained

Table 1

Selected geometric parameters (Å, °).

O1A-C11	1.194 (5)	O2A-C21	1.199 (5)
O1B-C11	1.299 (5)	O2B-C21	1.307 (5)
O14 C11 C12 N11	27.6 (5)	O24 $C21$ $C22$ $N21$	21.6 (5)
VIA CIA CIA CIA	-27.0(3)	02A-C2I-C22-N2I	-31.0(3)
N11-C12-C13-C14	-72.4(5)	N21-C22-C23-C24	-66.6 (5)
C12-C13-C14-S11	-178.3(3)	C22-C23-C24-S21	-178.5(3)
C13-C14-S11-C15	-85.7 (4)	C23-C24-S21-C25	176.0 (3)

Experimental

The title compound was crystallized by slow evaporation, at room temperature, from an aqueous solution containing a 1:1 stoichiometric ratio of L-methionine and nitric acid.



Figure 1

The structures of the two independent molecules of (I), showing the atomic numbering scheme and 50% probability displacement ellipsoids (Johnson, 1976).

+ 0.1845P]

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

$D - H \cdot \cdot \cdot A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$O1B-H1B\cdots O23^{i}$	0.82	1.90	2.663 (4)	156
$O2B - H2B \cdot \cdot \cdot O12^{ii}$	0.82	1.85	2.615 (4)	154
$N11-H11C\cdots O1A^{iii}$	0.89	2.08	2.859 (4)	145
N11-H11A···O13	0.89	2.50	2.934 (5)	111
N11−H11A···O11	0.89	2.22	3.072 (4)	161
$N11-H11B\cdots O13^{iv}$	0.89	2.01	2.854 (5)	158
N21-H21A···O23	0.89	2.13	2.988 (4)	162
N21-H21A···O22	0.89	2.51	2.943 (5)	111
$N21 - H21B \cdots O22^{iv}$	0.89	2.00	2.840 (5)	157
$N21-H21C\cdots O2A^{v}$	0.89	2.10	2.867 (4)	144
N21−H21C···O11	0.89	2.59	3.028 (4)	111

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

All H atoms were placed in geometrically calculated positions and included in the refinement in a riding-model approximation, with $U_{\rm iso}$ equal to $1.2U_{\rm eq}$ of the carrier atom ($1.5U_{\rm eq}$ for methyl and NH₃ H atoms).

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, 1997); 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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