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Key indicators

Single-crystal X-ray study T = 296 K Mean σ (C–C) = 0.009 Å R factor = 0.033 wR factor = 0.104 Data-to-parameter ratio = 10.0

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

A new high-pressure phase of the title amino acid (systematic 2-ammonio-4-methylpentanoate), C₆H₁₃NO₂. name: reported, with one molecule per asymmetric unit, in contrast to the atmospheric pressure phase, (I), reported by Harding & Howieson [Acta Cryst. (1976). B32, 633-634], which has two molecules in the asymmetric unit. The packing consists of a double layer structure, similar to those of (I) and other amino acids with non-polar side chains.

A high-pressure polymorph of L-*a*-leucine

Comment

L- α -Leucine, one of the most common amino acids, has been reported in two different crystal forms, both of them at atmospheric pressure: a room-temperatura one, hereafter (I) (Harding & Howieson, 1976, Coll et al., 1986, Görbitz & Dalhus, 1996) and a higher-temperature one, (II), derived from the former through a phase transition at 353.2 K (Bougeard, 1983).

On measuring the high-pressure solubility of L- α -leucine in water at room temperature (298.2 K), we found a breaking point in the solubility-pressure curve around 200 MPa. (Matsuo et al., 2002) Prismatic crystals 3-4 mm in size were observed as a residue of the process. Such large crystals, which proved to be stable for at least three years at ambient conditions because of hysteresis, could not be obtained by annealing the stable monoclinic form (I) at atmospheric pressure. In addition, its infrared spectrum differed from those of (I) and (II), therefore confirming it as a new phase, [hereafter (III)], the crystal structure of which we report here.



Fig. 1, the molecular structure of (III), shows the extended conformation adopted, which maximizes the distance of the methyl to the polar groups. Each ammonium group forms hydrogen bonds to three different molecules (Fig. 2 and Table 2), with typical $N-H \cdots O$ head-to-tail interactions. The three kinds of hydrogen bonds hold the carboxylate and ammonium groups together in double layers parallel to the ab plane, while the nonpolar groups stand alongside each other. The double layer structure is very similar to those of (I) and other amino acids with non-polar side chains such as L-valine

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(Torii & Iitaka, 1970), L-methionine (Torii & Iitaka, 1973), Lcystine (Harding & Long, 1968) and L-isoleucine (Torii & Iitaka, 1971). However, bifurcated hydrogen bonds reported in phase (I) are not present in the structure of phase (III). As a result of the packing scheme, some short non-hydrogenbonded N···O distances arise [2.731 (8) Å for N1···O2 (intramolecular distance), 3.44 (10) Å for N1···O1($x + \frac{1}{2}, y - \frac{1}{2},$ z) and 3.354 (6) Å for O2···N1($-x + \frac{3}{2}, y + \frac{1}{2}, -z + 1$)].

A few further characteristics differentiating (I) and (III) are *e.g.* the Z' values [1 for (III), 2 for (I)] and the X-ray diffraction density [1.173 g cm⁻³ for (III), 1.162 g cm⁻³ for (I)]. The latter difference is a direct consequence of the Le Chatelier principle: at higher pressure, a more compact crystal packing is preferred.

Experimental

L- α -Leucine was produced by Ajinomoto Co. A mixture of the leucine and water (1:1 in weight) was put in a pressure vessel and then pressed at 400 MPa and room temperature for a day. After the pressure was released, crystals were taken out, rinsed with acetone and then dried in a vacuum desiccator.

Crystal data

 $C_6H_{13}NO_2$ $M_r = 131.17$ Monoclinic, C2 a = 8.807 (3) Å b = 5.975 (1) Å c = 14.193 (3) Å $\beta = 96.17$ (2)°

Data collection

Rigaku AFC-5S diffractometer Absorption correction: ψ scan (North *et al.*, 1968) $T_{\min} = 0.738$, $T_{\max} = 0.868$ 1570 measured reflections 834 independent reflections

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.033$	83
$wR(F^2) = 0.104$	H-a
S = 1.50	$\Delta \rho$
834 reflections	$\Delta \rho$

Table 1

Selected bond lengths (Å).

O1-C2	1.248 (8)	C1-C3	1.528 (3)
O2-C2	1.250 (17)	C3-C4	1.526 (4)
N1-C1	1.493 (3)	C4-C5	1.525 (17)
C1-C2	1.530 (9)	C4-C6	1.526 (5)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$N1 - H13 \cdots O1^{i}$	0.94	1.97	2.890 (10)	165
$N1-H12\cdots O1^{ii}$	0.95	1.99	2.884 (2)	156
$N1-H11\cdots O2^{iii}$	0.96	1.73	2.680 (8)	179

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

 $V = 742.5 (3) Å^{3}$ Z = 4Cu K\alpha radiation $\mu = 0.72 \text{ mm}^{-1}$ T = 296 (2) K $0.40 \times 0.40 \times 0.20 \text{ mm}$

756 reflections with $F^2 > 2\sigma(F^2)$ $R_{int} = 0.024$ 3 standard reflections every 150 reflections

intensity decay: 2.9%

83 parameters
H-atom parameters not refined
$\Delta \rho_{\rm max} = 0.17 \ {\rm e} \ {\rm \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.15 \ {\rm e} \ {\rm \AA}^{-3}$



Figure 1

The molecular structure of L- α -leucine. Displacement ellipsoids are drawn at the 50% probability level.



Figure 2

A crystal packing diagram of (III), viewed approximately along the b axis. Hydrogen bonds are shown by lines in combined colors of red and light blue. H atoms not involved in hydrogen bonds have been omitted.

H atoms were placed at idealized positions (and kept fixed during refinement), at 0.95 Å from the host atom and completing a tetrahedral arrangement around it; in the case of CH₃ and NH₃ groups, H atoms were set in a *gauche* position to the host's next-nearest neighbors. In all cases, $U_{iso}(H) = 1.2U_{eq}(host)$. Since anomalous scattering effects were too small to provide a reliable indication of the absolute configuration, which is known for this compound, Friedel pairs were averaged.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1988); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *TEXSAN* (Molecular Structure Corporation, 2004); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *TEXSAN*; molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *TEXSAN*.

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