

**Data collection**

Syntex P4 four-circle diffractometer	$R_{\text{int}} = 0.066$
$\theta/2\theta$ scans	$\theta_{\text{max}} = 27.5^\circ$
Absorption correction: none	$h = -18 \rightarrow 17$
2204 measured reflections	$k = -5 \rightarrow 1$
1554 independent reflections	$l = -1 \rightarrow 14$
512 observed reflections [ $F > 4.0\sigma(F)$ ]	3 standard reflections monitored every 97 reflections
	intensity decay: 0.0001%

**Refinement**

Refinement on $F$	$\Delta\rho_{\text{max}} = 0.26 \text{ e } \text{\AA}^{-3}$
$R = 0.0470$	$\Delta\rho_{\text{min}} = -0.25 \text{ e } \text{\AA}^{-3}$
$wR = 0.0475$	Extinction correction: none
$S = 1.06$	Atomic scattering factors from <i>International Tables for Crystallography</i> (1992), Vol. C, Tables 4.2.6.8 and 6.1.1.4)
512 reflections	
119 parameters	
$w = 1/[\sigma^2(F) + 0.0008F^2]$	
$(\Delta/\sigma)_{\text{max}} = 0.001$	

Table 1. Fractional atomic coordinates and equivalent isotropic displacement parameters ( $\text{\AA}^2$ )

$$U_{\text{eq}} = (1/3)\sum_i \sum_j U_{ij} a_i^* a_j^* a_i \cdot a_j$$

	$x$	$y^\dagger$	$z$	$U_{\text{eq}}$
O1	0.5038 (3)	0.069 (1)	0.3570 (4)	0.043 (3)
N1	0.4001 (4)	0.294 (1)	0.4548 (5)	0.046 (4)
C2	0.3328 (5)	0.435 (2)	0.4922 (6)	0.039 (4)
N3	0.2928 (5)	0.623 (2)	0.3985 (5)	0.046 (4)
C4	0.3254 (5)	0.587 (2)	0.3056 (6)	0.039 (4)
N4	0.4442 (5)	0.278 (1)	0.2938 (5)	0.036 (3)
C5	0.3959 (5)	0.365 (2)	0.3516 (7)	0.032 (4)
C11	0.2214 (6)	0.793 (2)	0.3926 (7)	0.039 (4)
C12	0.1789 (6)	0.964 (2)	0.2987 (7)	0.051 (4)
C13	0.1084 (6)	1.140 (2)	0.2973 (8)	0.059 (5)
C14	0.0779 (7)	1.150 (2)	0.3877 (9)	0.059 (5)
C15	0.1167 (6)	0.976 (2)	0.4782 (9)	0.062 (5)
C16	0.1876 (6)	0.805 (2)	0.4829 (7)	0.046 (5)

$\dagger$  The small  $b$  cell dimension is reflected in high errors in the  $y$  atomic coordinates.

Table 2. Selected geometric parameters ( $\text{\AA}$ ,  $^\circ$ )

C11—N3	1.37 (1)	N4—O1	1.421 (8)
C11—C12	1.40 (1)	C4—C5	1.51 (1)
C11—C16	1.41 (2)	C5—N1	1.32 (1)
C12—C13	1.39 (2)	C5—N4	1.29 (1)
C13—C14	1.38 (2)	N1—C2	1.47 (1)
C14—C15	1.37 (2)	N3—C2	1.45 (1)
C15—C16	1.37 (2)	N3—C4	1.44 (1)
C4—N3—C2	113.8 (7)	C12—C11—N3	122.5 (9)
N3—C4—C5	101.6 (7)	C16—C11—N3	120.8 (8)
C4—C5—N1	109.8 (8)	C11—C12—C13	120.8 (10)
C4—C5—N4	121.1 (8)	C12—C13—C14	121.1 (9)
N1—C5—N4	129.1 (7)	C13—C14—C15	118.6 (10)
C5—N1—C2	113.7 (7)	C14—C15—C16	121.5 (11)
N3—C2—N1	100.9 (7)	C11—C16—C15	121.1 (9)
C5—N4—O1	108.9 (6)	C11—N3—C4	123.3 (7)
C12—C11—C16	116.7 (9)	C11—N3—C2	122.3 (8)

The H atom associated with the oxime O1 atom was located from a difference Fourier synthesis and the remaining H atoms were placed in sites with idealized geometry. All H atoms were included in least-squares cycles with fixed positional and isotropic displacement parameters. A variable scan rate was used, with a scan width of  $0.6^\circ$  below  $K\alpha_1$  and  $0.6^\circ$  above  $K\alpha_2$  to a maximum  $2\theta$  value of  $60^\circ$ . Refinement was completed using full-matrix least-squares methods.

Data collection: XSCANS (Siemens, 1991). Cell refinement: XSCANS. Data reduction: XSCANS. Program(s) used to solve structure: SHELXS86 (Sheldrick, 1990). Program(s) used to refine structure: SHELXS86. Molecular graphics: XP (Siemens, 1990).

Lists of structure factors, anisotropic displacement parameters, H-atom coordinates and complete geometry have been deposited with the IUCr (Reference: PA1215). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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**L-Isoleucine, Redetermination at 120 K**

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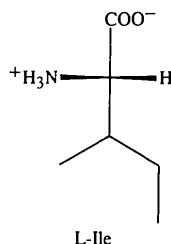
**Abstract**

This redetermination of L-isoleucine, C<sub>6</sub>H<sub>13</sub>NO<sub>2</sub>, forms part II in the series of crystal structures of hydrophobic amino acids. Standard deviations for bond lengths between heavy atoms are down to 0.002 Å. Detailed parameters for the hydrogen-bonding pattern are given.

**Comment**

The hydrophobic amino acids, except L-alanine, crystallize in monoclinic space groups with alternating hydro-

philic and hydrophobic layers, and almost identical hydrogen-bonding patterns. This makes them suitable as a database for multivariate analysis of hydrogen-bond parameters. We have undertaken a program to provide high-precision X-ray structures of these compounds. The first paper in the series describing the results of this investigation dealt with the structures of L-valine and L-methionine (Dalhus & Görbitz, 1996). The structure of L-isoleucine (L-Ile) was first determined by Torii & Iitaka (1971) with  $R = 0.117$  and standard deviations for bond lengths between heavy atoms in the range 0.011–0.018 Å. The current low-temperature study is considerably more accurate with standard deviations of 0.002–0.003 Å.



The asymmetric unit of L-Ile, with two crystallographically independent molecules *A* and *B*, is shown in Fig. 1. All deviations between analogous bond lengths in the polar parts of the two molecules are  $\leq 0.005$  Å (Table 2). The most important difference, also observed for L-Val and L-Met, lies in the carboxylate group, which is symmetric in molecule *A*, but asymmetric in molecule *B* with C—O bond lengths differing by 0.014 Å ( $7\sigma$ ) and bond angles  $C2B-C1B-O1B = 115.7(2)^\circ$  and  $C2B-C1B-O2B = 118.4(2)^\circ$ . The difference in the C2—C3 bonds observed by Torii & Iitaka (1971), 1.537 and 1.570 Å, was considered to be rather significant, but is not found at low temperature. As for the side chains, Fig. 1 reveals more extensive thermal motion in L-Ile(*B*), resulting in slightly shorter calculated bond lengths. This librational effect is particularly evident for the C3—C6 bond, which is 1.532(3) Å for L-Ile(*A*) with  $U_{eq}(C6A) = 0.022 \text{ \AA}^2$  and 1.518(3) Å for L-Ile(*B*) with  $U_{eq}(C6B) = 0.052 \text{ \AA}^2$ .

The conformations of L-Ile(*A*) and L-Ile(*B*) are very similar to those of the corresponding molecules in L-Val (Dalhus & Görbitz, 1996). For the corresponding torsion angles there are no deviations larger than  $1.4^\circ$  between the two structures. As in L-Val(*A*), the side chain of L-Ile(*A*) is significantly twisted relative to the ideal staggered positions at the  $C^\alpha-C^\beta$  bond, giving somewhat unusual values for the torsion angles with  $N1A-C2A-C3A-C4A = -155.0(2)^\circ$  and  $N1A-C2A-C3A-C6A = 79.4(2)^\circ$ .

Hydrogen-bond parameters are given in Table 3. The hydrogen-bond pattern and the crystal packing are strikingly similar to those observed previously for L-Met and L-Val (Dalhus & Görbitz, 1996).

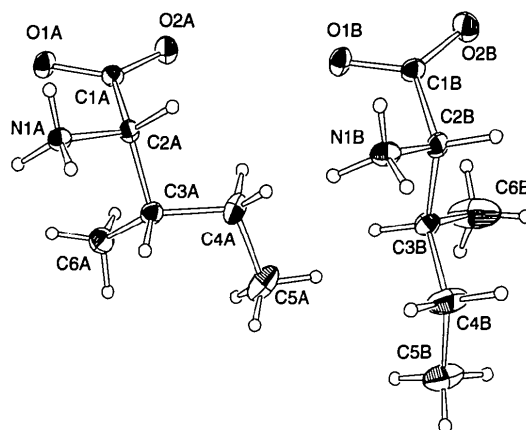


Fig. 1. The asymmetric unit with atomic numbering (ORTEP; Johnson, 1976). Displacement ellipsoids are shown at the 50% probability level. H atoms are shown as spheres of arbitrary size.

## Experimental

The title compound was obtained from Sigma Corporation and used without further refinement. Crystals were grown by slow cooling of a warm saturated aqueous solution.

### Crystal data

$C_6H_{13}NO_2$   
 $M_r = 131.17$   
 Monoclinic  
 $P2_1$   
 $a = 9.681(5) \text{ \AA}$   
 $b = 5.301(3) \text{ \AA}$   
 $c = 13.956(6) \text{ \AA}$   
 $\beta = 96.16(4)^\circ$   
 $V = 712.1(6) \text{ \AA}^3$   
 $Z = 4$   
 $D_x = 1.224 \text{ Mg m}^{-3}$   
 $D_m$  not measured

Mo  $K\alpha$  radiation  
 $\lambda = 0.71069 \text{ \AA}$   
 Cell parameters from 25 reflections  
 $\theta = 12.5\text{--}17.5^\circ$   
 $\mu = 0.091 \text{ mm}^{-1}$   
 $T = 120(2) \text{ K}$   
 Plate  
 $1.00 \times 0.50 \times 0.05 \text{ mm}$   
 Colourless

### Data collection

Nicolet P3 diffractometer  
 $2\theta$  scans  
 Absorption correction: none  
 3431 measured reflections  
 3431 independent reflections  
 2738 observed reflections  
 $[I > 2\sigma(I)]$

$\theta_{max} = 35.0^\circ$   
 $h = -15 \rightarrow 15$   
 $k = 0 \rightarrow 8$   
 $l = 0 \rightarrow 22$   
 3 standard reflections monitored every 96 reflections  
 intensity decay: none

### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.0524$   
 $wR(F^2) = 0.1316$   
 $S = 1.009$   
 3430 reflections  
 205 parameters  
 All H-atom parameters refined  
 $w = 1/[\sigma^2(F_o^2) + (0.0809P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{max} = 0.003$   
 $\Delta\rho_{max} = 0.422 \text{ e \AA}^{-3}$   
 $\Delta\rho_{min} = -0.270 \text{ e \AA}^{-3}$   
 Extinction correction: none  
 Atomic scattering factors from *International Tables for Crystallography* (1992, Vol. C, Tables 4.2.6.8 and 6.1.1.4)

Table 1. Fractional atomic coordinates and equivalent isotropic displacement parameters (Å<sup>2</sup>)

$$U_{eq} = (1/3)\sum_i \sum_j U_{ij} a_i^* a_j^* \mathbf{a}_i \cdot \mathbf{a}_j$$

	x	y	z	$U_{eq}$
O1A	0.11628 (11)	-0.0167 (3)	0.41256 (9)	0.0177 (3)
O2A	0.18514 (12)	0.3602 (3)	0.36350 (10)	0.0195 (3)
N1A	0.36618 (14)	-0.2275 (3)	0.41995 (11)	0.0149 (3)
C1A	0.2055 (2)	0.1312 (3)	0.38363 (12)	0.0139 (3)
C2A	0.34707 (15)	0.0176 (3)	0.36696 (11)	0.0133 (3)
C3A	0.3628 (2)	-0.0190 (4)	0.25875 (12)	0.0160 (3)
C4A	0.4075 (2)	0.2312 (5)	0.21567 (15)	0.0260 (4)
C5A	0.4308 (3)	0.2170 (6)	0.10901 (15)	0.0363 (6)
C6A	0.2304 (2)	-0.1279 (4)	0.20399 (13)	0.0222 (3)
O1B	0.62713 (12)	0.5636 (3)	0.40883 (9)	0.0175 (2)
O2B	0.70429 (15)	0.9557 (3)	0.38462 (11)	0.0241 (3)
N1B	0.88872 (15)	0.3764 (3)	0.39427 (10)	0.0182 (3)
C1B	0.7143 (2)	0.7198 (4)	0.38167 (12)	0.0156 (3)
C2B	0.8385 (2)	0.6041 (3)	0.33698 (12)	0.0158 (3)
C3B	0.7967 (2)	0.5281 (4)	0.23100 (12)	0.0179 (3)
C4B	0.9163 (2)	0.4018 (6)	0.18619 (14)	0.0338 (6)
C5B	0.8842 (2)	0.3372 (6)	0.07956 (15)	0.0369 (6)
C6B	0.7421 (4)	0.7567 (6)	0.17339 (15)	0.0536 (9)

Table 2. Selected geometric parameters (Å, °)

O1A—C1A	1.264 (2)	O1B—C1B	1.269 (2)
O2A—C1A	1.257 (2)	O2B—C1B	1.255 (2)
N1A—C2A	1.497 (2)	N1B—C2B	1.500 (2)
C1A—C2A	1.537 (2)	C1B—C2B	1.540 (2)
C2A—C3A	1.546 (2)	C2B—C3B	1.544 (2)
C3A—C6A	1.532 (3)	C3B—C6B	1.518 (3)
C3A—C4A	1.537 (3)	C3B—C4B	1.528 (3)
C4A—C5A	1.531 (3)	C4B—C5B	1.526 (3)
O2A—C1A—O1A	125.0 (2)	O2B—C1B—O1B	125.8 (2)
O2A—C1A—C2A	117.73 (15)	O2B—C1B—C2B	118.4 (2)
O1A—C1A—C2A	117.2 (2)	O1B—C1B—C2B	115.7 (2)
N1A—C2A—C1A	109.27 (13)	N1B—C2B—C1B	109.09 (14)
N1A—C2A—C3A	110.72 (14)	N1B—C2B—C3B	109.72 (15)
C1A—C2A—C3A	112.31 (13)	C1B—C2B—C3B	110.85 (13)
C6A—C3A—C4A	112.7 (2)	C6B—C3B—C4B	111.7 (2)
C6A—C3A—C2A	111.71 (14)	C6B—C3B—C2B	109.9 (2)
C4A—C3A—C2A	109.6 (2)	C4B—C3B—C2B	111.97 (14)
C5A—C4A—C3A	114.5 (2)	C5B—C4B—C3B	114.4 (2)
O1A—C1A—C2A—N1A	-19.0 (2)	O1B—C1B—C2B—N1B	-41.4 (2)
N1A—C2A—C3A—C6A	79.4 (2)	N1B—C2B—C3B—C6B	178.4 (2)
N1A—C2A—C3A—C4A	-154.95 (14)	N1B—C2B—C3B—C4B	-56.9 (2)
C2A—C3A—C4A—C5A	178.3 (2)	C2B—C3B—C4B—C5B	-176.4 (2)

Table 3. Hydrogen-bonding geometry (Å, °)

D—H...A	D—H	H...A*	H...A†	D...A	D—H...A*
N1A—H1A...O2A <sup>i</sup>	0.92 (3)	1.95(3)	1.841	2.859 (2)	170 (2)
N1A—H2A...O1B <sup>j</sup>	0.89 (3)	1.89(3)	1.751	2.778 (2)	175 (3)
N1A—H3A...O1B <sup>ii</sup>	0.86 (2)	2.07(2)	1.931	2.839 (2)	148 (2)
N1B—H1B...O2B <sup>j</sup>	0.93 (4)	1.94(4)	1.837	2.851 (3)	168 (3)
N1B—H2B...O2A <sup>iii</sup>	0.85 (3)	2.13(3)	1.961	2.948 (2)	161 (4)
N1B—H2B...O1A <sup>iii</sup>	0.85 (3)	2.35(4)	2.230	3.023 (2)	136 (3)
N1B—H3B...O1A <sup>iv</sup>	0.85 (2)	1.91(3)	1.735	2.760 (2)	174 (2)

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

\* Experimental H-atom positions. † Normalized (Taylor & Kennard, 1983) hydrogen bonds with  $d(\text{N—H}) = 1.030 \text{ \AA}$ .

Amino-group H atoms were refined isotropically, other H atoms were placed geometrically. Refinement then allowed the H atoms to move along the C—H bond direction with the C—H distance being kept constant for all H atoms on the same C atom. The  $U_{iso}$  values were fixed at  $1.2 \times U_{eq}$  of the bonded atom, except that a free variable for  $U_{iso}$  was refined for each of the four methyl groups.

Program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994). Program(s) used to refine structure: *SHELXL93* (Sheldrick, 1993). Molecular graphics: *ORTEPII* (Johnson, 1976).

Lists of structure factors, anisotropic displacement parameters, H-atom coordinates and complete geometry have been deposited with the IUCr (Reference: HA1156). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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## 1,3-Adamantanedicarboxylic Acid and 1,3-Adamantanediactic Acid

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## Abstract

The structure of 1,3-adamantanedicarboxylic acid (tricyclo[3.3.1.1<sup>3,7</sup>]decane-1,3-dicarboxylic acid), C<sub>12</sub>H<sub>16</sub>O<sub>4</sub>, consists of hydrogen-bonded chains of molecules related by a glide plane. In 1,3-adamantanediactic acid (tricyclo[3.3.1.1<sup>3,7</sup>]decane-1,3-diacetic acid), C<sub>14</sub>H<sub>20</sub>O<sub>4</sub>, the asymmetric unit comprises two hydrogen-bonded molecules and these bimolecular units are in turn linked by hydrogen bonds across centres of inversion to give chains.

## Comment

The crystal structures of dicarboxylic acids in which the two acidic functions are at sites remote from one another on a rigid three-dimensional framework exhibit a range of hydrogen-bonding patterns. The structures of bicyclo[2.2.2]octane-1,4-dicarboxylic acid (Ermer &