2-Butenylglycine Hydrochloride

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Abstract. $C_6H_{11}NO_2$. HCl, $M_r = 165.5$, monoclinic, $P2_1/c, a = 12.506 (15), b = 6.471 (5), c = 10.826 (12)$ Å, $\beta = 98.91 (5)^{\circ}$, Z = 4. $D_m = 1.27$, $D_x = 1.269$ Mg m⁻³. Final R = 0.11. The compound exists in the trans form. The structure is loosely packed and the Cl⁻ ion has three alternative disordered sites of low occupancy and a predominant large-occupancy site. The side-chain conformation does not correspond to other reported methionine structures.

Introduction. Biological antagonists owe their action to their close structural similarity to normal metabolites. Analyses of the hydrochloride of *p*-nitrophenylalanine (Chacko, Swaminathan, Parthasarathy & Natarajan, 1978), an antagonist of phenylalanine, and of thienylserine (Swaminathan & Chacko, 1979), an antagonist of serine and threonine have been reported. The hydrochloride of 2-butenylglycine (I), an antagonist of methionine, could have a cis or trans conformation about the $C^{\nu}-C^{\delta}$ bond. X-ray analysis was necessary to establish the conformation. It has been shown (Skinner, Edelson & Shive, 1961) that the cis form of (I) is a more effective competitive antagonist of methionine in E. coli than the trans form.



Flat, plate-like crystals were formed from a solution of 2-butenylglycine in dilute hydrochloric acid supplied by Nutritional Biochemicals Corporation, USA. Preliminary studies were carried out with Weissenberg photographs. The cell dimensions were determined from the 2θ values of 30 reflections on a Picker fourcircle diffractometer (Cu Ka radiation, $\lambda = 1.54178$ Å, $\mu = 3.50 \text{ mm}^{-1}$). A crystal $0.1 \times 0.2 \times 0.2 \text{ mm}$ was used for data collection with b coinciding with the

 φ axis. The θ -2 θ scan mode was employed with 2° min⁻¹ scan speed. The scan range was 2° with backgrounds measured on either side of the peak for 10 s. 1407 reflections were measured with $I > 2\sigma(I)$ within the range $2\theta \leq 130^{\circ}$. The data were corrected for Lorentz and polarization factors and initially scaled by Wilson's method.

The Cl atom was located from a Patterson map (R = 0.5). A Fourier synthesis revealed all the nonhydrogen atoms and also showed that the side-chain of this amino acid exists in the trans form. The structure was refined isotropically with the blockdiagonal least-squares program of Shiono (1968) to an R of 0.16. A difference map computed at this stage showed three small (<2 e Å⁻³) peaks close to the Cl atom, indicative of disorder. The intensities (as well as the initial Weissenberg photographs) showed that the reflections were unusually weak for a heavy-atom derivative and also indicated possible disorder. Further, the low density indicated that the structure was loosely packed.

By introducing these extra peaks with partial occupancy factors there was a significant drop in R to 0.14. The partial occupancy factors for the three alternative positions were near 0.085 with the main Cl atom (predominant position) having an occupancy of 0.745. Further refinement was carried out with the full-matrix program LALS (Gantzel, Sparks & Trueblood, 1961) with isotropic temperature factors for the disordered

Table 1. The final positional parameters $(\times 10^4)$ of non-hydrogen atoms

	x	У	z
C(1)	1328 (4)	8364 (7)	551 (5)
C(2)	1537 (4)	7086 (8)	1737 (5)
C(3)	2736 (5)	6788 (9)	2256 (5)
C(4)	3339 (5)	5595 (12)	1376 (6)
C(5)	3769 (5)	3743 (14)	1594 (7)
C(6)	4339 (6)	2509 (13)	730 (9)
N	977 (3)	5053 (6)	1451 (4)
O(1)	726 (3)	7855 (6)	-367 (3)
O(2)	1909 (4)	10082 (6)	685 (4)
CI	1448 (2)	1770 (3)	3656 (1)
Cl'	1078 (14)	1837 (19)	3609 (12)
Cl″	1821 (16)	1800 (19)	3717 (13)
Cl'''	1442 (10)	2954 (26)	3666 (11)

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Cl atom and anisotropic temperature factors for other non-hydrogen atoms. The H atoms located from the difference map were included in fixed positions. The occupancy factors of the disordered Cl were also fixed. Refinement converged to R = 0.11. Hughes (1941) weights were used $(1/w^2$, where $w = |F_o|$ for $|F_o| \ge 4.0$ and w = 4.0 for $|F_o| < 4.0$).

Scattering factors were taken from International Tables for X-ray Crystallography (1962) and an f' (= 0.3) correction was applied to Cl⁻. Tables 1 and 2* give the final atomic parameters (these correspond to the L-configuration).

Discussion. The bond lengths and angles (Fig. 1) compare well with standard values. The carboxyl group exists as COOH with the N atom in the NH⁺₃ state and

* Lists of structure factors and anisotropic thermal parameters have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 33918 (8 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 2. H atom positions $(\times 10^3)$ and isotropic temperature factors

	x	у	z	B (Å ²)
H(1)N	90	418	225	4.67
H(2)N	17	520	130	4.67
H(3)N	125	407	75	4.67
H(4)O(2)	176	1117	-2	4.78
H(5)C(2)	121	798	239	2.82
H(6)C(3)	308	837	237	2.45
H(7)C(3)	283	601	315	2.45
H(8)C(4)	341	637	49	4.39
H(9)C(5)	367	299	248	4.65
H(10)C(6)	520	299	80	5.01
H(11)C(6)	398	81	98	5.01
H(12)C(6)	398	273	-20	5.01



Fig. 1. Bond lengths (Å) and angles (°).

chloride as Cl^- . As is usual in amino acids, the C=O [C(1)-O(1)] bond occurs *cis* to N.

As expected the non-polar side chain of (I) shows a gradual increase in temperature factors (and e.s.d.'s in positional parameters) with a minimum for C^{α} [C(2)], gradually increasing to a maximum for C^{ε} [C(6)].

The carboxyl group C(1), C(2), O(1) and O(2) are coplanar with N deviating from the plane by 0.190 Å (Table 3, plane 1). The atoms involved in the double bond C(4)=C(5) are essentially planar [C(3), C(4), C(5) and C(6)] (Table 3, plane 2).

Torsion angles representing the backbone and sidechain conformations are given in Table 4. C(3) and C(6)are *trans* with respect to C(4)=C(5). The χ^2 angle of 246.1° does not occur in any of the staggered conformations (60, 180, 300°) generally observed for the amino acid side chains (Lakshminarayanan, Sasisekharan & Ramachandran, 1967). This peculiarity is attributed to the double bond C(4)=C(5) which necessarily restricts the side-chain conformation. Table 4 also gives the torsion angles of other methionine structures: the α - and β -forms of DL-methionine (Mathieson, 1952), L-methionine (Torii & Iitaka, 1973) and Lmethionine. HCl (Di Blasio, Pavone & Pedone, 1977). Table 4 shows that χ^2 is generally near 180° except for (I) and for the B molecule of L-methionine. For β methionine and for L-methionine (A molecule) the

Table 3. Least-squares-plane calculations

Deviations are in Å $\times 10^3$.

Plane 1: C(1), C(2), O(1) and O(2) 0.814x - 0.468y - 0.343z = -1.457Deviations: C(1) -2, C(2) 1, O(1) 1, O(2) 1, N 190

Plane 2: C(3), C(4), C(5) and C(6) 0.809x + 0.418y + 0.412z = 5.304Deviations: C(3) 9, C(4) -9, C(5) -10, C(6) 10



Fig. 2. Projection of the structure down b.

Table 4. Torsion angles (°)

IUPAC-IUB		2-Butenylglycine			L-Methionine		L-Methionine
designation		HCI	α -Methionine	β -Methionine	A Molecule	B Molecule	HCl
ψ^1	N-C(2)-C(1)-O(1)	7.3 (6)	-33.7	-29.4	-17.5	-34.3	0
χ ¹	N-C(2)-C(3)-C(4)	57.9 (6)	299.9	299.0	194.0	194.4	61
χ^2	C(2) - C(3) - C(4) - C(5)	246.1 (7)	176.9	183.6	174.2	73.6	182
χ^3	C(3)-C(4)-C(5)-C(6)	178.2 (7)	80.5	190-4	179.7	73.6	69

Table 5. Hydrogen-bond distances (Å) and angles (°)

$D-H\cdots A$	$D \cdots A$	$\mathbf{H}\cdots \mathbf{A}$	$\angle D$ —H···A
$N-H(1)\cdots Cl$	3.18	2.21	153
$N-H(2)\cdots Cl^{a}$	3.22	2.27	157
$N-H(2)\cdots O(1)^d$	2.96	2.42	112
$N-H(3)\cdots Cl^{b}$	3.38	2.38	153
$O(2) - H(4) \cdots Cl^{c}$	2.99	1.95	179
Symmetry code			
(a) $-x$, $\frac{1}{2} + y$, $\frac{1}{2}$ (b) x , $\frac{1}{2} - y$, $\frac{1}{2} + z$	-z (c) -1 (d)	$x, \frac{1}{2} - y + x, 1 - y$	$+1, \frac{1}{2}+z-1 \\ -y, \qquad -z$

 χ^3 angle shows that C^{β} and the terminal methyl C^{ϵ} are *trans* to each other as observed for (I). Table 4 shows that in none of the structures is the *cis* conformation observed (*i.e.* χ^3 close to 0°).

A view of the molecule down b is given in Fig. 2. The alternative Cl positions of low occupancy are given by dots and are approximately in a plane parallel to (001).

Table 5 gives the hydrogen-bond distances and angles referred to the predominant Cl position. H(1) and H(3) of NH₃⁺ are hydrogen bonded to symmetryrelated Cl⁻ ions (Cl and Cl^b) at $D \cdots A$ distances of 3.18 and 3.38 Å respectively. H(2) of N forms a bifurcated hydrogen bond with Cl^a and O(1)^d at $D \cdots A$ distances of 3.22 and 2.95 Å respectively. Table 5 shows that (for the bifurcated hydrogen bond) the distances H(2) to Cl^a and O(1)^d are 2.27 and 2.42 Å respectively and the latter distance suggests that it is a weak interaction. The hydroxyl O(2) forms a hydrogen bond with Cl^c at a distance of 2.99 Å.

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