

The Crystal Structure and the Absolute Configuration of (+)-2-Benzylglutamic Acid Hydrobromide Dihydrate*¹

Tamaichi ASHIDA, Yoshio SASADA*² and Masao KAKUDO

Institute for Protein Research, Osaka University, Joancho, Kita-ku, Osaka

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The crystal structure of (+)-2-benzylglutamic acid hydrobromide dihydrate has been determined using three-dimensional X-ray intensity data. The crystal is orthorhombic, with four formula units in a unit cell with the dimensions: $a=8.38$, $b=10.54$, and $c=17.68$ Å, the space group being $P2_12_12_1$. The structure was solved by the heavy atom method, and its parameters were refined by the least-squares method using anisotropic thermal parameters, the final R being 0.073. The absolute configuration of the glutamic acid has also been determined to be D-(+)-2-benzylglutamic acid, $[\alpha]_D^{20} +1.65^\circ$ (c 10, 4 N HCl). The conformation of the carbon skeleton of the glutamic acid is different from any of the glutamic acids so far analyzed, due to the internal rotations of the C—C bonds. A detailed comparison of the conformations of several glutamic acids and glutamines will be given. Nine independent hydrogen bonds make a rather unique and complicated three-dimensional network. Among these, two between the carboxyl groups (donor) and the water molecules (acceptor) are found to be fairly strong, their bond lengths being 2.55 and 2.51 Å.

Recently, Izumi and his collaborators¹⁻⁴⁾ have extensively investigated the asymmetric hydrogenation of methyl acetoacetate to methyl 3-hydroxybutyrate. They have used Raney nickel catalysts, modified under various conditions, with several optically active compounds, such as amino acids and hydroxy acids. α -C-substituted glutamic acids, such as 2-methyl- and 2-benzylglutamic acid, were also tested as the modifying reagents; the natures of the activities of the catalysts modified by them have been found to be quite different from that of the catalyst with L-glutamic acid.⁴⁾ Thus, levorotatory methyl 3-hydroxybutyrate is obtained by the catalyst modified with (+)-2-methylglutamic acid, and the dextrorotatory product with (+)-2-benzylglutamic acid; while by the catalyst modified with L-glutamic acid, the direction of the optical rotation of the product is much influenced by the pH and by the temperature of the modifying solution. The determination of the absolute configuration of such α -C-substituted glutamic acids as well as their steric conformations are necessary in order to study the mechanism of such asymmetric reactions. DL-2-Benzylglutamic

acid was newly synthesized, and its optical resolution was performed by Izumi and his collaborators.⁵⁾ The optical rotation of (+)-2-benzylglutamic acid was $[\alpha]_D^{20} +1.65^\circ$ (c 10, 4 N HCl).

2-Benzylglutamic acid is characterized by the lack of a hydrogen atom on the asymmetric α -carbon atom. Though the crystal structures of many amino acids have been studied, the structural analyses of α -C-dialkyl glycines have been rather few; the only example is α -aminoisobutyric acid.⁶⁾ The substituted groups, a propionic acid residue and a benzyl group, in 2-benzylglutamic acid are, however, quite a bit larger than the two methyl groups in α -aminoisobutyric acid; thus the crowded surroundings of the α -carbon atom in 2-benzylglutamic acid are rather interesting from the viewpoint of structural chemistry. The crystal structures of β -glutamic acid,⁷⁾ glutamic acid hydrochloride,⁸⁾ glutamine⁹⁾ and glutathione¹⁰⁾ have already been reported; the effect of the substitution of a large group on the conformation of glutamic acid will also be clarified by the structure analysis of the present compound. On the other hand, the present amino acid is phenylalanine with a propionic acid residue substituted at the α -carbon atom. Phenylalanine is a rare example of a substance the crystal structure of which has not

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*² Present address: Faculty of Science, Tokyo Institute of Technology, Ookayama, Meguro-ku, Tokyo.

1) Y. Izumi, M. Imaida, H. Fukawa and S. Akabori, *This Bulletin*, **36**, 21 (1963).

2) Y. Izumi, M. Imaida, H. Fukawa and S. Akabori, *ibid.*, **36**, 155 (1963).

3) S. Tatsumi, M. Imaida, Y. Fukuda, Y. Izumi and S. Akabori, *ibid.*, **37**, 846 (1964).

4) Y. Izumi, S. Tatsumi, M. Imaida, Y. Fukuda and S. Akabori, *ibid.*, **38**, 1206 (1965).

5) Y. Izumi, S. Tatsumi, M. Imaida, Y. Fukuda and S. Akabori, *ibid.*, **38**, 1338 (1965).

6) S. Hirokawa, S. Kuribayashi and I. Nitta, *ibid.*, **25**, 192 (1952).

7) S. Hirokawa, *Acta Cryst.*, **8**, 637 (1955).

8) B. Dawson, *ibid.*, **6**, 81 (1953).

9) W. Cochran and B. R. Penfold, *ibid.*, **5**, 644 (1952).

10) W. B. Wright, *ibid.*, **11**, 632 (1958).

yet been reported, though one peptide, glycyl-phenylalanyl-glycine,¹¹⁾ has been reported on.

The present paper will deal with the crystal structure of (+)-2-benzylglutamic acid hydrobromide dihydrate as determined and refined by three-dimensional X-ray analysis. The absolute configuration of the amino acid will also be determined using the anomalous dispersion effect of the bromine atom.

Experimental

The crystals of (+)-2-benzylglutamic acid hydrobromide were obtained from its aqueous solution as rods elongated along the *a* axis. They were kindly supplied by Professor Yoshiharu Izumi of this Institute. The unit cell dimensions were obtained from Weissenberg photographs about the principal axes. The powder-diffraction patterns of aluminum were superimposed on the photographs as a standard. The dimensions are:

$a = 8.28 \pm 0.02$, $b = 10.54 \pm 0.02$, and $c = 17.68 \pm 0.02$ Å. From the systematic absences of $h00$, $0k0$ and $00l$ for h , k and l odd, the space group was found to be $P2_12_12_1$. The density of the crystal, as measured by the flotation method, was 1.515 g cm^{-3} , whereas the calculated value was 1.37 g cm^{-3} on the basis of four formula units per cell. A good agreement between the observed and the calculated values was obtained by assuming two crystallization water molecules per asymmetric unit; the calculated value thus became 1.525 g cm^{-3} . The presence of the crystallization water was later confirmed by the chemical analysis; thus the crystal was found to be (+)-2-benzylglutamic acid hydrobromide dihydrate.

Three-dimensional intensity data were collected from the equi-inclination Weissenberg photographs, using $\text{CuK}\alpha$ radiation. The crystals were rotated around the *a* axis ($h=0$ to 6) and the *b* axis ($k=0$ to 4). Intensities were measured visually by comparison with a standard scale; they ranged from 1 to 15000 on an arbitrary scale. A total of 1786 reflections were obtained, of which 107 were too weak to be estimated. They were corrected for Lorentz and polarization factors, and the spot-shape correction given by Phillips¹²⁾ was applied to the elongated spots. No absorption corrections were made, though they seemed necessary because of the large linear absorption coefficient for $\text{CuK}\alpha$ radiation, $\mu = 42.2 \text{ cm}^{-1}$; the cross sections of the crystals used in the experiments were both about $0.015 \times 0.01 \text{ cm}$.

Structure Determination

The coordinates of the bromide ion were determined from the Patterson function projected on the *a* and *b* axes. The three-dimensional electron-density function was then synthesized, using all the observed reflections with phases assigned by the bromide ion. Though there appeared several false peaks of heights comparable with those of carbon atoms, a set of coordinates of all the atoms,

including two water molecules, was established without difficulty. Using the coordinates of all the non-hydrogen atoms thus obtained, the structure factors were then calculated for all the observed reflections; the error index, $R = \sum |F_o - F_c| / \sum F_o$, was 0.23. In the second three-dimensional electron-density map the structure showed up clearly.

The structure was subjected to least-squares refinement using the block-diagonal matrix approximation. In the first step all the atoms were treated as isotropic; after two cycles the error index decreased from 0.20 to 0.14. Then all the non-hydrogen atoms were assigned with anisotropic thermal parameters; the reflections used in the refinement were those with $\sin \theta / \lambda$ values of less than 0.55 (1237 reflections). After several cycles,

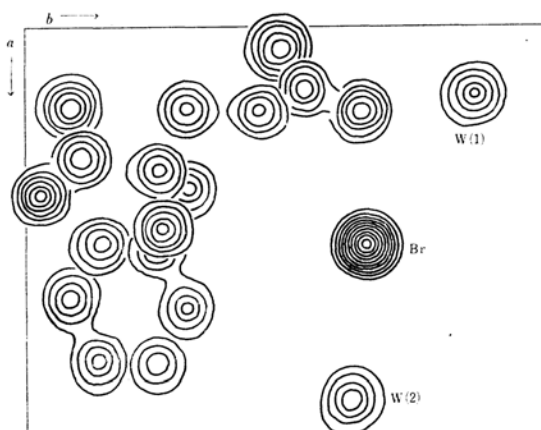


Fig. 1. A composite drawing of the final electron-density map, viewed along the *c* axis. Contours are at intervals of 2 e. \AA^{-3} , beginning with the 2 e. \AA^{-3} contour. For Br, contours are at intervals of 6 e. \AA^{-3} beginning with 6 e. \AA^{-3} .

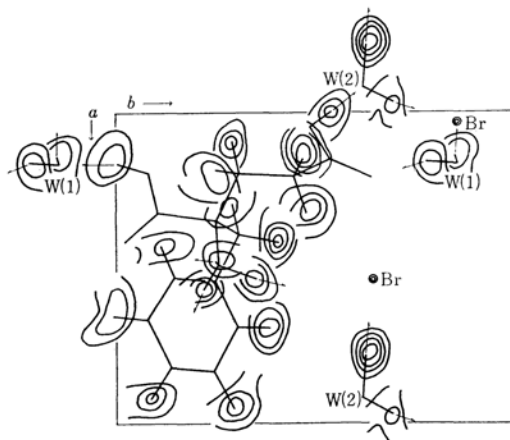


Fig. 2. A composite drawing of the final difference map, viewed along the *c* axis. The contributions of the hydrogen atoms were omitted from the structure factor calculations. Contours are at intervals of 0.15 e. \AA^{-3} , beginning with the 0.15 e. \AA^{-3} contour.

11) R. E. Marsh and J. P. Glusker, *ibid.*, **14**, 1110 (1961).

12) D. C. Phillips, *ibid.*, **9**, 819 (1956).

R decreased to 0.079. At this stage, the difference Fourier function was synthesized using these 1237 reflections. Several residual peaks with heights of from 0.3 to 0.7 e.Å⁻³ appeared, and most

of them were found at the sites where hydrogen atoms were expected to be present. Finally, all the hydrogen atoms with isotropic temperature factors were included in the refinement; the error

TABLE I.

(a) Atomic coordinates (in fraction of cell edges) and their standard deviations in 10⁻³ Å

Atom	x	$\sigma(x)$	y	$\sigma(y)$	z	$\sigma(z)$	Atom	x	$\sigma(x)$	y	$\sigma(y)$	z	$\sigma(z)$
Br	0.5337	1	0.6500	1	0.0522	1	C(3)	0.1997	10	0.3058	9	0.2628	9
O(1)	0.1964	7	0.0839	6	0.1724	7	C(4)	0.2048	11	0.4478	9	0.2785	9
O(2)	0.4133	7	0.0278	6	0.2388	6	C(5)	0.1502	10	0.5338	9	0.2139	9
O(3)	0.0447	8	0.4867	6	0.1679	7	C(6)	0.3946	10	0.3082	9	0.1459	9
O(4)	0.2032	7	0.6425	7	0.2078	7	C(7)	0.5441	11	0.2500	8	0.1105	7
W(1)	0.1660	9	0.8610	7	0.1245	7	C(8)	0.6924	11	0.3051	9	0.1232	10
W(2)	0.9212	8	0.6229	9	0.0638	8	C(9)	0.8329	12	0.2481	11	0.0926	9
N	0.4945	8	0.2635	7	0.2760	7	C(10)	0.8218	11	0.1356	10	0.0512	9
C(1)	0.3226	10	0.1056	8	0.2128	8	C(11)	0.6702	12	0.0809	10	0.0385	9
C(2)	0.3504	10	0.2506	8	0.2243	8	C(12)	0.5321	11	0.1394	10	0.0675	7

(b) Temperature factors in form of

$$\exp\{-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + \beta_{12}hk + \beta_{13}hl + \beta_{23}kl)\}$$

Atom	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
Br	0.0208	0.0108	0.0023	0.0018	0.0003	-0.0011
O(1)	0.0130	0.0047	0.0032	-0.0011	-0.0049	-0.0001
O(2)	0.0142	0.0035	0.0028	0.0024	-0.0019	-0.0003
O(3)	0.0166	0.0056	0.0036	-0.0035	-0.0083	0.0009
O(4)	0.0147	0.0038	0.0034	-0.0024	-0.0032	0.0015
W(1)	0.0288	0.0043	0.0029	-0.0039	-0.0043	0.0000
W(2)	0.0176	0.0131	0.0044	-0.0004	-0.0058	0.0033
N	0.0098	0.0045	0.0021	-0.0004	-0.0022	0.0009
C(1)	0.0109	0.0033	0.0020	-0.0016	0.0011	0.0003
C(2)	0.0109	0.0034	0.0018	0.0015	0.0006	0.0008
C(3)	0.0111	0.0049	0.0018	-0.0005	0.0017	0.0002
C(4)	0.0121	0.0050	0.0022	0.0013	-0.0000	0.0008
C(5)	0.0105	0.0050	0.0027	0.0012	0.0001	-0.0015
C(6)	0.0125	0.0052	0.0019	0.0013	-0.0004	0.0030
C(7)	0.0135	0.0046	0.0013	-0.0012	-0.0004	0.0007
C(8)	0.0132	0.0053	0.0027	-0.0020	0.0024	0.0006
C(9)	0.0152	0.0074	0.0024	-0.0029	0.0023	-0.0010
C(10)	0.0153	0.0077	0.0020	-0.0011	0.0018	0.0016
C(11)	0.0208	0.0074	0.0022	-0.0005	0.0026	-0.0016
C(12)	0.0129	0.0073	0.0018	-0.0013	-0.0012	0.0002

(c) Atomic coordinates and isotropic temperature factors for the hydrogen atoms

Atom	x	y	z	B	Atom	x	y	z	B
H(1)	0.161	0.002	0.162	3.8	H(11)	0.190	0.252	0.316	3.1
H(2)	0.000	0.541	0.129	3.9	H(12)	0.147	0.466	0.324	2.6
H(3)	0.154	0.776	0.145	5.2	H(13)	0.327	0.481	0.296	2.9
H(4)	0.137	0.857	0.078	5.0	H(14)	0.295	0.292	0.106	2.8
H(5)	0.801	0.634	0.059	4.5	H(15)	0.417	0.410	0.154	2.3
H(6)	0.965	0.701	0.033	5.9	H(16)	0.697	0.392	0.158	2.3
H(7)	0.533	0.358	0.274	2.9	H(17)	0.950	0.293	0.098	2.6
H(8)	0.560	0.227	0.257	3.8	H(18)	0.925	0.089	0.028	4.1
H(9)	0.484	0.249	0.328	3.2	H(19)	0.662	0.995	0.003	2.0
H(10)	0.099	0.289	0.236	1.9	H(20)	0.432	0.107	0.059	4.3

TABLE 2. OBSERVED AND CALCULATED STRUCTURE FACTORS
($\times 5$)

[illegible]

In order to establish the absolute configuration of the glutamic acid, the anomalous dispersion effect due to the bromine atom was used. Though the effect is small for the $\text{CuK}\alpha$ radiation ($\Delta f' = -0.9$ and $\Delta f'' = 1.5$),¹⁴⁾ about 30 pairs of F_{H} and F_{H} values were found to show fairly significant differences, ($F_{\text{H}} - F_{\text{H}}$). 32 pairs of reflections were used in the calculations; all but two indicated that the glutamic acid has the D-configuration. The structure factors calculated on the basis of the D-configuration by using $\Delta f' = -0.9$ and $\Delta f'' = 1.5$ are listed in Table 3, together with their

TABLE 3. OBSERVED AND CALCULATED STRUCTURE FACTORS ($\times 10$) USED FOR THE DETERMINATION OF THE ABSOLUTE CONFIGURATION

h	k	l	Obs.		Calcd.		h	k	l	Obs.		Calcd.	
			F_H	$F_{\bar{H}}$	F_H	$F_{\bar{H}}$				F_H	$F_{\bar{H}}$	F_H	$F_{\bar{H}}$
1	1	2	66	95	51	79	3	1	8	64	52	68	51
1	1	7	117	96	111	90	3	1	9	59	46	60	48
1	2	11	92	103	92	96	3	2	4	41	46	41	48
1	2	19	59	52	62	57	3	3	6	52	42	55	50
1	3	3	71	66	77	55	3	5	1	94	87	94	91
1	3	7	63	57	76	70	4	1	5	133	152	115	133
1	3	10	56	61	54	63	4	1	6	124	112	115	101
1	3	12	103	96	97	87	4	1	9	101	120	99	114
1	4	9	57	73	60	67	4	2	2	137	112	142	136
2	1	10	96	105	94	101	4	2	6	116	94	110	87
2	1	14	112	123	118	129	4	2	8	94	105	99	104
2	1	16	131	126	146	138	4	2	15	84	77	103	95
2	2	7	68	77	76	79	4	3	2*	98	89	89	90
2	3	7	156	140	151	139	4	4	1	114	92	112	94
2	7	1	64	59	74	67	5	1	9*	71	81	76	75
3	1	1	123	131	130	146	6	1	3	52	43	54	46

* See text.

TABLE 4. BEST PLANES

(a) Coefficients for the planes. Each plane is represented by $lX + mY + nZ + p = 0$, where X , Y and Z are coordinates in Å.

Plane	l	m	n	p	
1	0.5545	0.0317	-0.8316	1.6072	(α -carboxyl group)
2	0.7414	-0.3457	-0.5751	3.2053	(γ -carboxyl group)
3	-0.0997	0.5379	-0.8371	0.6604	(phenyl group)
4	-0.9521	0.0295	0.3045	0.2824	(three neighbors of W(1))
5	0.0417	-0.7205	-0.6922	5.7364	(three neighbors of W(2))

(b) Displacements of atoms from the planes (Å)

Plane 1		Plane 2		Plane 3		Plane 4		Plane 5	
O(1)	0.002	O(3)	-0.002	C(7)	-0.007	O(4)	0	O(3)	0
O(2)	0.002	O(4)	-0.003	C(8)	-0.004	O(1)	0	W(2)'	0
C(1)	-0.006	C(4)	-0.002	C(9)	0.010	Br	0	Br	0
C(2)	0.002	C(5)	0.007	C(10)	-0.007	W(1)*	-0.09	W(2)*	0.199
N*	-0.094	C(3)*	0.643	C(11)	-0.004				
C(3)*	-1.239			C(12)	0.013				
C(6)*	1.376			C(6)*	-0.077				

* Shows that the atom was not included in the evaluation of the equation of the plane.

observed structure factors, the two pairs indicating another configuration being marked by asterisks; the error index for these 64 reflections is 0.076. Thus this amino acid was determined to be D-(+)-2-benzylglutamic acid, as is shown in Fig. 3. This configuration is also favored by Izumi and his collaborators from their studies of the asymmetric syntheses.¹⁵⁾

15) Y. Izumi, Private communication.

Discussion

All the bond distances, angles and other important intra- and intermolecular approaches below 4.0 Å were calculated from the atomic coordinates listed in Table 1, and the equations of the best planes of several planar groups were evaluated, the latter being listed in Table 4. These computations were performed on the HITAC 5020 at the

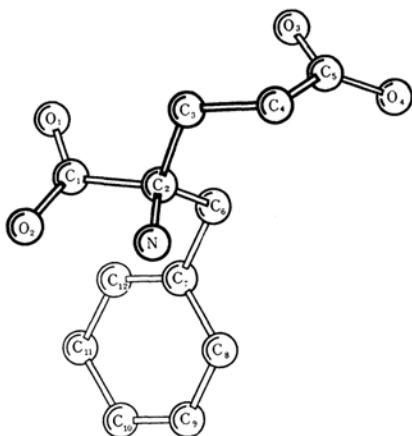


Fig. 3. The absolute configuration: D-(+)-2-benzylglutamic acid.

University of Tokyo using a program written by the present authors.

Figure 4 shows the bond distances and angles in the present glutamic acid. The standard deviations of the bond lengths and angles among C, N and O are from 0.010 to 0.017 Å and from 0.7° to 1.0° respectively. The C(2)–NH₃⁺ bond distance, 1.51 Å, is a little longer than the average value, 1.493 Å,^{*3} found in many amino acids, but

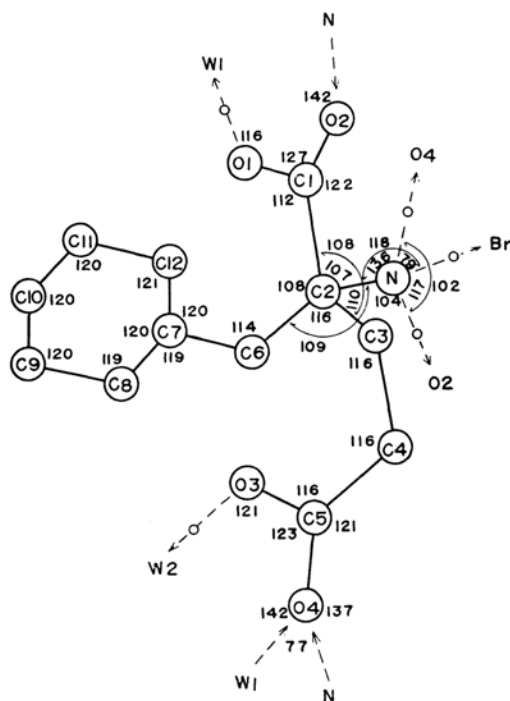


Fig. 4(b).

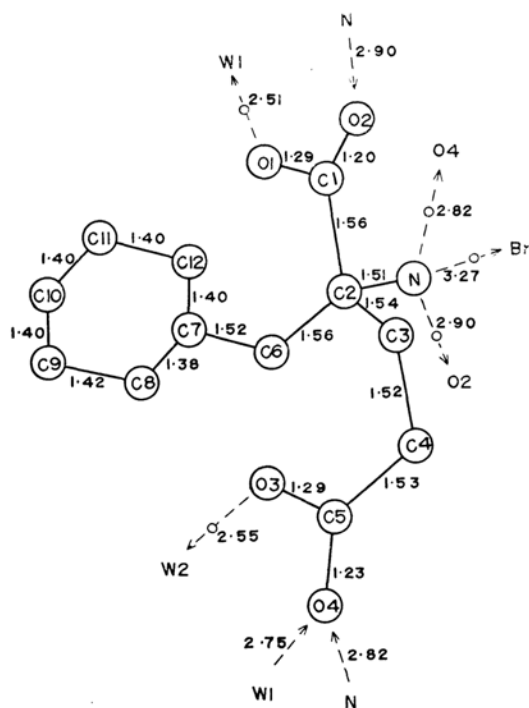


Fig. 4(a).

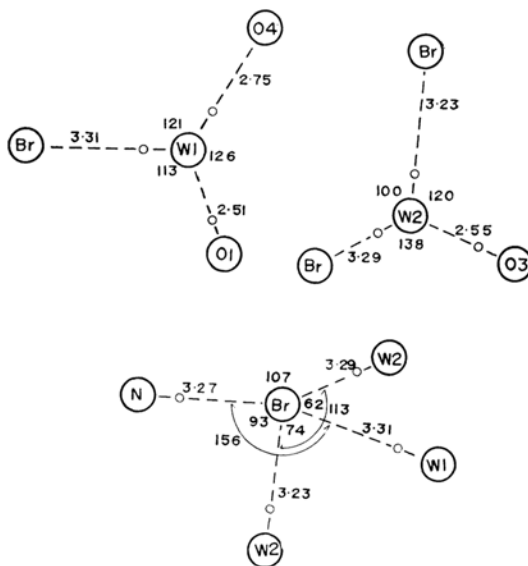


Fig. 4(c).

Fig. 4. Bond lengths (Å) and angles (°). The broken lines show the hydrogen bonds.

*3 This is the average of the C–NH₃⁺ bond distances in amino acids, the crystal structures of which have been analyzed by using three-dimensional intensity data.

the difference may not be significant. The nitrogen atom is nearly coplanar with the α -carboxyl group, the displacement of the atom from the plane being 0.09 Å. The C–C single bonds range from 1.52 to 1.56 Å, which are quite normal. Also normal are the shape and the size of the phenyl group; the C–C bond lengths range from 1.38 to

1.42 Å, with an average of 1.40 Å, while the bond angles range from 119° to 121°. The group is planar, as is shown in Table 4.

There are some interesting and significant variations in the bond angles in the carbon skeleton of the present glutamic acid. The bond angles, C(2)–C(6)–C(7) (114°), C(2)–C(3)–C(4) (116°), and C(3)–C(4)–C(5) (116°), are significantly larger than the regular tetrahedral angles, but such large differences are not so unusual in such substances. The C(6)–C(2)–C(3) angle, 116°, is also large, but the other five bond angles around the C(2) atom are all close to 109.5°. Among the four substituents of the C(2) atom, the propionic acid residue and the benzyl group are much larger than the α -carboxyl and the α -amino groups. Thus the wide angle of C(6)–C(2)–C(3) is due to the repulsion force between the two large substituents; the bond angles around C(3), C(4) and C(6) mentioned above may also have a somewhat similar significance. The dimensions of two

carboxyl groups are almost equal to each other. O(1) and O(3) have hydrogen atoms, and C(1)–O(1) and C(5)–O(3) are both 1.29 Å. The bond distances of C(1)–O(2), 1.20 Å, and C(5)–O(4), 1.23 Å, are close to the length of the pure double bond between the carbon and the oxygen atom; O(4) is the acceptor of two hydrogen bonds, while O(2) accepts only one. In general, these carboxyl groups are very similar to those found in glutamic acid hydrochloride^{8b} and in many carboxylic acids.

Hirokawa^{7d} gave an interesting discussion of the carbon-chain configurations in β -glutamic acid,^{7d} glutamic acid hydrochloride^{8b}, and glutamine.^{9d} Since then, the structure of glutathione (γ -L-glutamyl-L-cysteinyl-glycine) has been determined;¹⁰ thus, it may be of some significance to extend his discussion by including the present crystal and the glutamyl residue in glutathione. In Fig. 5, the molecular configurations in the five crystals are shown for the sake of comparison. We can summarize the following features:

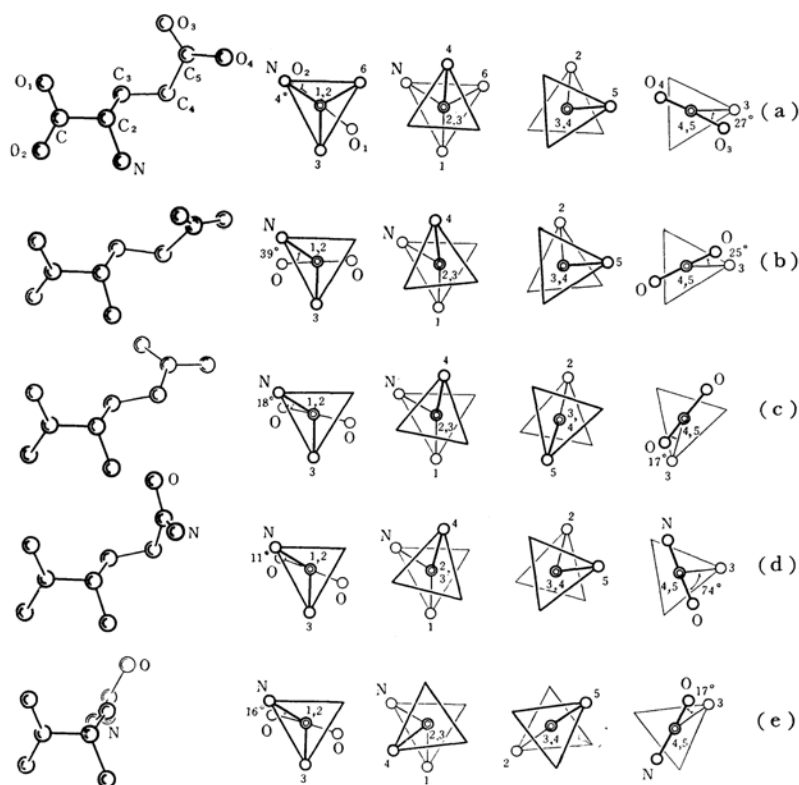


Fig. 5. Carbon-chain configurations of some related compounds. The first column shows molecules viewed down the planes of C'–C α –N (C(1)–C(2)–N). In the second to the last, the arrangements of atoms nearest to the particular bonds are shown. The second shows α -carboxyl, α -N, C β , H α and two H β 's viewed down the C α –C' bond, the third down the C β –C α , and so on. The bold lines show the atoms on the upper side, and the positions of hydrogen atoms are idealized. The triangles of N, C' and H α have the same orientation in all the molecules, and the orientations of the others are correlating with the first. L-Amino acids are figured for all the molecules. A part of the figure is after Hirokawa.^{7d} (a) present crystal, (b) β -glutamic acid, (c) glutamic acid hydrochloride, (d) glutathione, (e) glutamine.

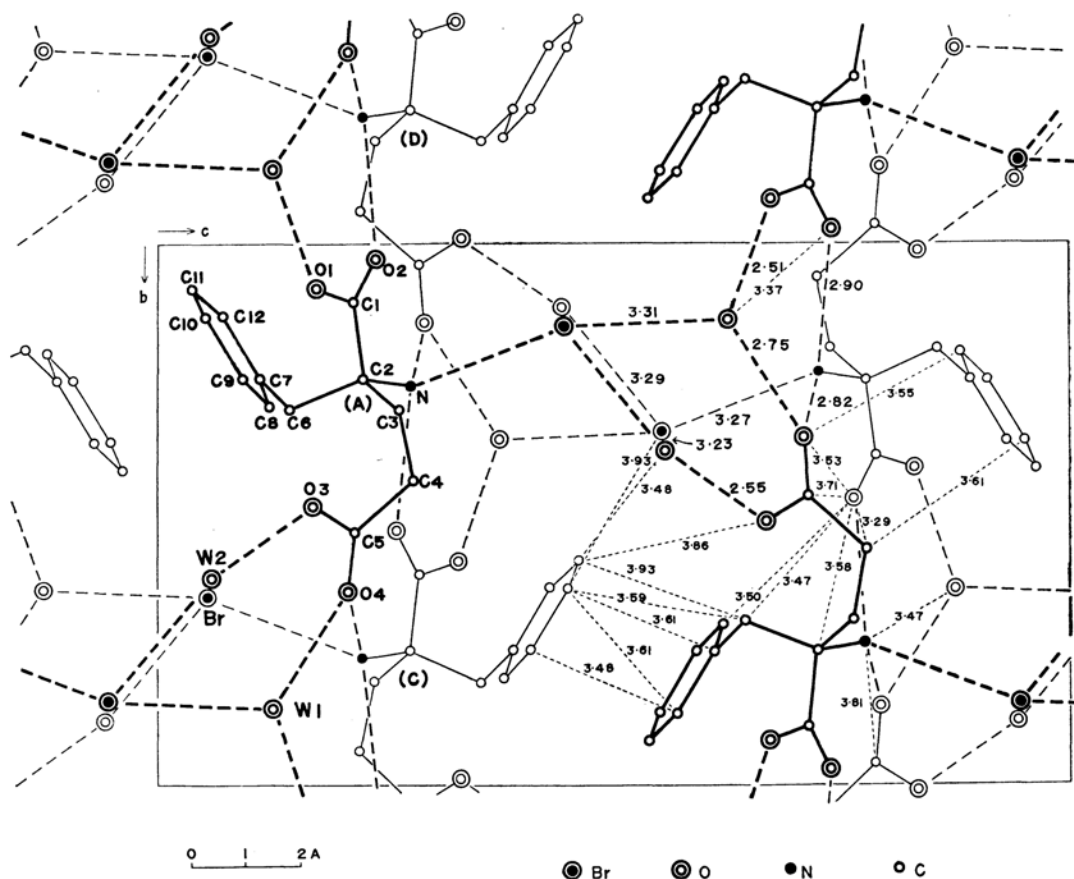


Fig. 6. A drawing of the structure viewed along the *a* axis. The broken lines show the hydrogen bonds. Some of the short intermolecular approaches are shown.

(1) The arrangement of C(1), α -N and C(4) about the C(2)–C(3) bond causes one of the most distinct differences in the molecular configurations. This is the case not only in these amino acids, but also in all the other amino acids and peptides. Recently Ramachandran and Lakshminarayanan¹⁶⁾ have found some systematic tendencies (maybe rules) in the relative arrangements of the α -carboxyl, α -amino groups and γ -atoms around the C_α – C_β bonds in some amino acids and peptides in the crystals.*⁴ Among the present amino acids, C(4) is in the gauche position to both C(1) and α -N in glutamine, while in the other four, C(4) is in the trans position to C(1) and gauche to α -N. From the viewpoint of Ramachandran and Lakshminarayanan, therefore, the latter seems to be a rule for glutamic acids. No rules, however, can be found for glutamines, because glutathione is an *N*-substituted glutamine.

16) G. N. Ramachandran and A. V. Lakshminarayanan, *Biopolymers*, **4**, 495 (1966).

*⁴ In this report C(2) corresponds to C_α in the usual nomenclature for the atoms in amino acids, and so on.

(2) The displacements of the α -N atoms from the carboxyl planes are 0.09, 0.82, 0.43, 0.35, and 0.28 Å in the present crystal, β -glutamic acid, glutamic acid hydrochloride, glutamine, and glutathione respectively; thus α -N is nearly coplanar with the carboxyl group in the present crystal, but in the other four the displacements are significant.

(3) C(2) and C(5) can be in either the trans or the gauche position about the C(3)–C(4) bond. The side chain in glutamic acid hydrochloride is roughly planar, including C(1) and C(2), and in glutamine the side chain and C(2) are roughly coplanar, while in the other three the side chains are not planar because of the internal rotations of the C(3)–C(4) bonds.

(4) The angles between the two planes, C(3)–C(4)–C(5), and the γ -carboxyl groups (or the amide groups in glutamine and glutathione) are not very large except in the case of glutathione; in the latter the large size may be due to the rather large side group in the cysteinyl residue.

(5) Thus, no pairs of the five molecules are essentially the same. The differences are due to

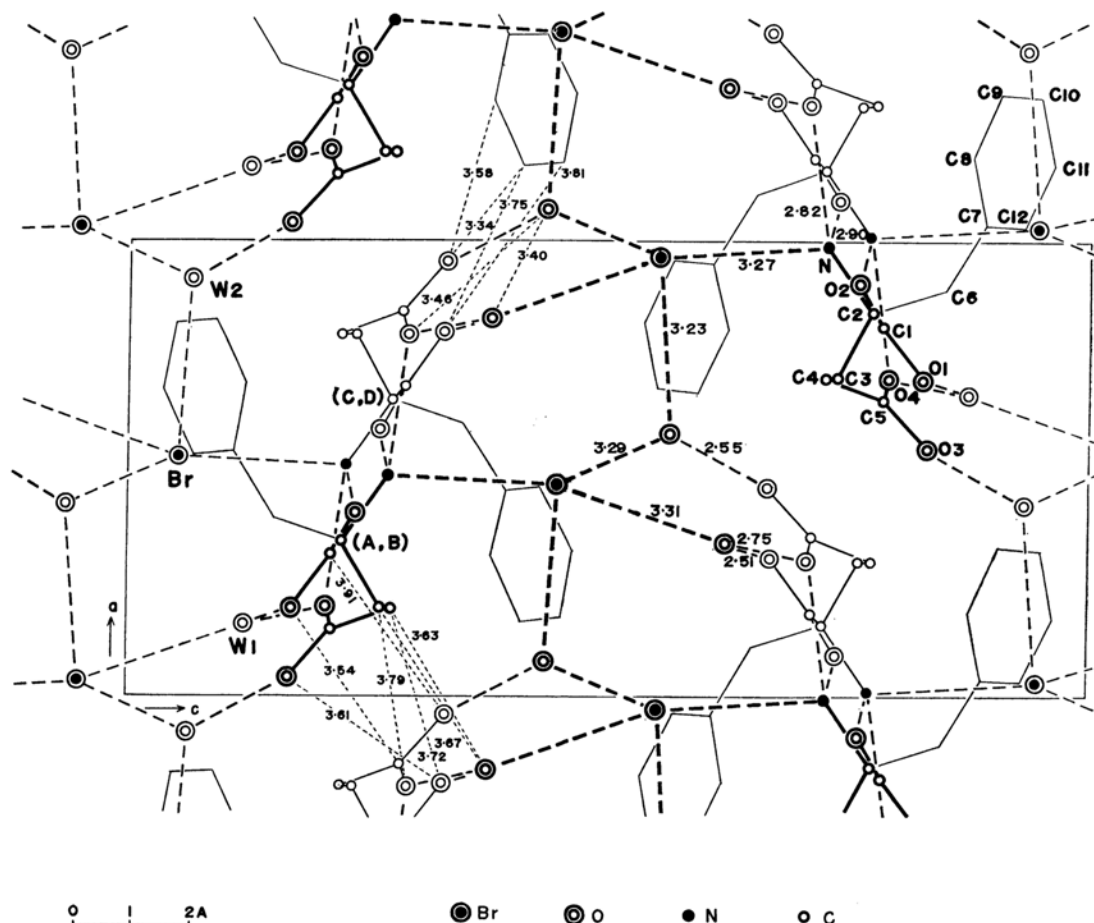


Fig. 7. A drawing of the structure viewed along the b axis.

the internal rotations of all the C-C bonds.

The arguments given above support the conclusion of Hirokawa¹⁷ that the carbon-chain configurations in the related compounds depend more or less on the effects of the surrounding molecules, especially on the modes of hydrogen bonds at the terminal groups. Analogous situations may be expected in aspartic acid and asparagine; however, there are not yet enough data on these amino acids. A similar "polymorphism of the molecular configurations" due to the hydrogen bonds has been found not only in other amino acids (for example, arginine dihydrate, arginine monohydrochloride monohydrate, and arginine monohydrochloride),¹⁷ but also in other compounds (*e.g.*, ethylenediamine and tetramethylenediamine).¹⁸ In other amino acids, methionine¹⁹ and isoleucine,²⁰ the configurations of the side chains have also been found to be different

in several crystal modifications, but this may be due to the van der Waals forces rather than to the hydrogen bonds.

The present amino acid is phenylalanine with a propionic acid residue substituted at the α -carbon atom. The phenyl group protrudes laterally from the glutamic acid residue. The dihedral angle between the phenyl and the α -carboxyl groups is 49° . In the review by Ramachandran and Lakshminarayanan¹⁶ mentioned above, it is found that C_7 in tyrosine and phenylalanine is in the trans position to α -N with respect to the C_α - C_β bond, while in tryptophan C_7 is in the gauche position to both the carboxyl group and α -N or in the trans position to the carboxyl group. Besides, in histidine (three crystals, hydrochloride salt²¹) and two Zn salts^{22,23})

20) J. Trommel and J. M. Bijvoet, *ibid.*, **7**, 703 (1954).

21) J. Donohue, L. R. Lavine and J. S. Rollett, *ibid.*, **9**, 655 (1956).

22) M. M. Harding and S. J. Cole, *ibid.*, **16**, 643 (1963).

23) R. H. Kretsinger, F. A. Cotton and R. F. Bryan, *ibid.*, **16**, 651 (1963).

17) G. N. Ramachandran, S. K. Mazumdar, K. Venkatesan and A. V. Lakshminarayanan, *J. Mol. Biol.*, **15**, 232 (1966).

18) T. Ashida and S. Hirokawa, *Acta Cryst.*, **16**, 841 (1963).

19) A. McL. Mathieson, *ibid.*, **5**, 332 (1952).

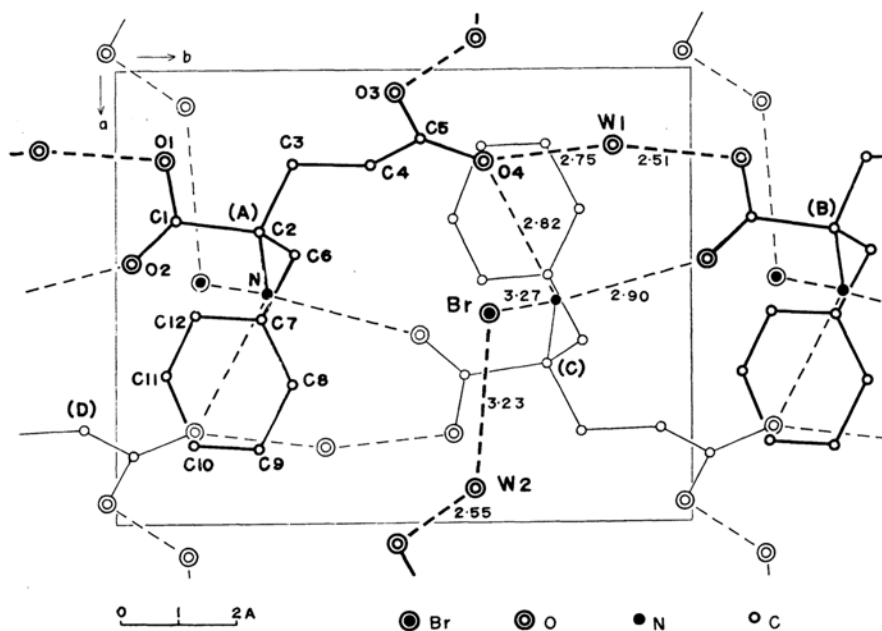


Fig. 8. A drawing of the structure viewed along the c axis. Only the contents between $z=0$ and $z=1/2$ are shown.

C_7 is in the gauche position to both the carboxyl group and α -N. Thus, there seems to be a difference in the conformations of atoms with respect to the C_α - C_β bond, according to whether C_7 belongs to the benzene ring or to the five-membered (basic) ring. In the present case, however, $C(7)^{*5}$ goes to the gauche position to both $C(1)$ and α -N with respect to the $C(2)$ - $C(6)$ bond. Perhaps the present case may be an exception, because $C(2)$ does not have a hydrogen atom, in contrast to the other amino acids and peptides.

Hydrogen Bonds and Molecular Packing.

There are nine independent hydrogen bonds in the crystal shown in Figs. 4, 6, 7 and 8. Among these, two hydrogen bonds between the non-ionized carboxyl groups (donors) and the water molecules (acceptors) seem to be fairly strong, their O—O distances being 2.55 and 2.51 Å. Very few hydrogen bonds of such a type have, however, been reported. A few of the examples which have been reported are 2.49 Å in oxalic acid dihydrate,²⁴⁾ and 2.537 and 2.503 Å in potassium tetraoxalate dihydrate.²⁵⁾ Thus, though there are not enough data, the hydrogen bonds between the carboxyl groups (donor) and the water molecules (acceptors) seem to be generally stronger than other types of hydrogen bonds between two oxygen atoms. The dimensions of

other hydrogen bonds found in the present crystal are comparable to those reported elsewhere.

The bromide ion is the acceptor of four hydrogen bonds, of which one is from the nitrogen atom, while three are from the water molecules. The arrangement of the four donor atoms of these hydrogen bonds around the bromide ion is far from being tetrahedral.

Two water molecules participate in three hydrogen bonds. Their nearest-neighbor coordinations are shown in Fig. 4c. As is shown in Table 4 and in Fig. 4c, both water molecules have nearly planar and trigonal environments. The displacements of $W(1)$ and $W(2)$ from the planes defined by their three neighbors are only 0.20 and 0.09 Å respectively. This is not unusual in hydrated structures; for example, such coordinations have been found in barbituric acid dihydrate,²⁶⁾ cytosine monohydrate,²⁷⁾ and dilituric acid trihydrate.²⁸⁾ As has been pointed out by Clark,²⁹⁾ in almost one quarter of the hydrated structures which have been studied the water molecules have planar threefold environments.

The packing scheme in the crystal is rather unique. Generally, in crystals composed of both polar and non-polar groups we have found layers of molecular contacts of polar or ionic parts and,

26) G. A. Jeffrey, S. Ghose and J. O. Warwicker, *ibid.*, **14**, 881 (1961).

27) G. A. Jeffrey and Y. Kinoshita, *ibid.*, **16**, 20 (1963).

28) B. M. Craven, S. Martinez-Carrera and G. A. Jeffrey, *ibid.*, **17**, 891 (1964).

29) J. R. Clark, *Rev. Pure Appl. Chem.*, **13**, 50 (1963).

*5 $C(6)$ and $C(7)$ correspond to C_β and C_γ respectively if the present amino acid is deemed to be phenylalanine.

24) F. R. Ahmed and D. W. J. Cruickshank, *ibid.*, **6**, 385 (1953).

25) D. J. Haas, *ibid.*, **17**, 1511 (1964).

alternately, molecular contacts composed of non-polar parts. However, this is not the case in the present crystal, there being no layers as such. Rather, there are, roughly speaking, three kinds of approaches between the molecules or the ions; the polar organic part (glutamic acid residue), non-polar organic part (phenyl group), and the part of the water molecule, W(2), and the bromide ion. Around the twofold screw axis at $y=1/4$ and $z=0$, there are only contacts among the phenyl groups due to the van der Waals forces. Around the other twofold screw axis, at $y=3/4$ and $z=0$, the bromide ion and the water molecule W(2) gather together and make a zigzag chain of hydrogen bonds elongated along the screw axis. Glutamic acid residues are located roughly at $z=1/4$ or $3/4$. As is shown in Figs. 6, 7 and 8, the A molecule at (x, y, z) is connected to B at $(x, 1+y, z)$ by the hydrogen bonds *via* the nitrogen atom of the C molecule at $(1-x, 1/2+y, 1/2-z)$ and *via* the W(1) water molecule. The A and C molecules are related to each other by the twofold screw axis at $x=1/2$ and $z=1/4$. Similarly, the C and D molecules are connected by A and other

W(1). Thus, these molecules make an column made of two rows of molecules elongated along the b axis. The contact between the columns along the a axis is due to the van der Waals forces. Besides, these columns are connected indirectly along the a and c axes by many hydrogen bonds *via* the bromide ions and the W(2) water molecules. Thus, the two water molecules and the bromide ion play an important role in building up the complicated three-dimensional network, rather than as spacers.

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