

Crystal and Molecular Structure of ω -Amino Acids, ω -Aminosulfonic Acids and Their Derivatives. III. The Crystal and Molecular Structure of γ -Guanidino- β -hydroxypropane Sulfonic Acid

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γ -Guanidino- β -hydroxypropane sulfonic acid $C_4H_{11}O_4N_3S$ crystallizes in the monoclinic space group $P2_1/c$, with four formula units in a unit cell of dimensions, $a=7.44$, $b=9.89$, $c=11.11$ Å and $\beta=97.75^\circ$. The crystal structure was determined by the heavy atom method and refined by block-diagonal least-squares to an R -value of 0.12 using intensity data collected photographically. The molecule takes the zwitterionic form, $(NH_2)_2^+CNH-CH_2CH(OH)CH_2SO_3^-$. The skeletal conformation of the molecule is planar *trans* zigzag. The molecules are held together in the crystal by a three-dimensional network of $NH\cdots O$ and $OH\cdots O$ hydrogen bonds.

γ -Guanidino- β -hydroxypropane sulfonic acid (GGBOPSA) is one of the derivatives of chemical transmitter in the central nervous system¹⁻³⁾ such as γ -aminobutyric acid (GABA), γ -amino- β -hydroxybutyric acid (GABOB), homotaurine and taurine. This work is a part of a series of structural studies on the derivatives of the above compounds. Details of action mechanisms are not clear. However, it was reported that guanidino derivatives of ω -aminosulfonic acid such as GGBOPSA and γ -guanidinopropane sulfonic acid (GGPSA) act as a depressant for the lowering of blood pressure, whereas homotaurine and γ -amino- β -hydroxypropane sulfonic acid (GABOPSA) show an excitatory action for it.⁴⁾ It would be of great interest to elucidate the correlation between structural specificities and biological implications of these compounds.

Some structural features of GGBOPSA and its related compounds have been reported.⁵⁾ This paper deals with the precise structure analysis of GGBOPSA and comparison of the molecular structure with that of the related compounds.

Experimental

A racemic sample of GGBOPSA (supplied by Prof. S. Tsunoo, Medical School of Showa University) was recrystallized from water at room temperature as colorless, transparent prisms elongated along the a -axis. The space group and cell constants were determined from Weissenberg and precession photographs. The crystal data are presented in Table 1. Intensity data of 1452 independent reflections around a and b -axes were collected from equi-inclination Weissenberg photographs by the multiple film method with $CuK\alpha$ radiation and estimated by visual comparison with a calibrated scale. Lorentz, polarization and spot-shape corrections were applied, but no absorption correction was made. The approximate scale factor and over-all temperature factor were calculated by Wilson's method.

Structure Determination and Refinement

The structure was solved by the usual heavy-atom procedure. By interpretation of high peaks on sharpened Patterson function, the coordinates of sulfur atom were easily determined. From the Fourier synthesis with only the heavy atom phase, all the non-hydrogen atoms could be found. R -index, $R=\sum||F_o|-|F_c||/\sum|F_o|$, was reduced from 0.32 to 0.18 by block-diagonal least-squares refinement with isotropic temperature factors, the unit weight being applied for the non-zero reflections. Refinement was continued with anisotropic temperature factors and R -index was reduced to 0.14. The used anisotropic temperature factors are of the form: $\exp\{-(B_{11}h^2+B_{22}k^2+B_{33}l^2+B_{12}hk+B_{13}hl+B_{23}kl)\}$.

A difference Fourier synthesis calculated in this stage revealed all the hydrogen atoms which were included in the further refinement. The final R -value was 0.12. The used atomic scattering factors were taken from *International Tables for X-ray Crystallography*.⁶⁾

All the computations were carried out on NEAC 2200-500 and 2200-700 machines at this University and on FACOM 230-60 at the University of Kyoto, using the programs of UNICS system.

Results and Discussion

The final positional and thermal parameters are listed in Tables 2-a and b, together with their estimated

TABLE 1. CRYSTAL DATA OF GGBOPSA

Molecular Formula: $C_4H_{11}O_4N_3S$	M.W.=197.21
Colorless transparent prism, Monoclinic system	
$a=7.44\pm0.02$ Å	$b=9.89\pm0.02$ Å
$c=11.11\pm0.03$ Å	$\beta=97.75\pm0.5^\circ$
Volume of the unit cell, 810.02 Å ³	
Density (by flotation) 1.621 g cm ⁻³	
Density (calculated) 1.617 g cm ⁻³	
$Z=4$	$F(000)=416$
Absent spectra: $h0l$ when $l=2n+1$	
$0k0$ when $k=2n+1$	
Space group, $P2_1/c$	

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2) A. N. Davison and L. K. Kaczmarek, *Nature*, **234**, 107 (1971).

3) T. Hayashi and K. Nagai, Proc. 20th Int. Physiol. Cong., (1956), Brussels, Belgium, p. 410.

4) S. Tsunoo, K. Horisaka, H. Tanaka, T. Chida, S. Nakajima, and Z. Fukai, *J. Showa Med. Assoc.*, **30**, 521 (1970).

5) Y. B. Kim, A. Wakahara, T. Fujiwara, and K. Tomita, *Chem. Lett.*, **1972**, 891.

6) "International Tables for X-ray Crystallography," Vol. 3, Kynoch Press, England (1962).

TABLE 2-a. FINAL POSITIONAL AND THERMAL PARAMETERS WITH THEIR ESTIMATED STANDARD DEVIATIONS IN PARENTHESES ($\times 10^4$)

The anisotropic temperature factors are expressed in the form of

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

Atom	x/a	y/b	z/c	B_{11}	B_{22}	B_{33}	B_{12}	B_{13}	B_{23}
S	12216(3)	950(2)	3718(2)	62(4)	18(2)	37(2)	-1(5)	44(4)	-25(3)
O(1)	12240(10)	-269(7)	2972(7)	111(14)	59(7)	82(7)	34(17)	41(16)	-111(12)
O(2)	13224(10)	2062(7)	3271(7)	86(13)	66(7)	84(7)	-38(17)	138(16)	13(12)
O(3)	12792(10)	671(7)	4996(6)	125(14)	42(6)	34(5)	20(15)	-30(13)	-1(9)
O(4)	10181(9)	3873(6)	3945(6)	86(13)	29(6)	64(6)	-30(14)	47(14)	-21(10)
C(1)	9914(12)	1461(9)	3591(8)	70(17)	30(7)	45(8)	30(19)	31(18)	-23(12)
C(2)	9597(12)	2679(8)	4408(8)	52(16)	25(7)	46(7)	-2(18)	23(17)	5(12)
C(3)	7640(13)	2772(9)	4561(9)	76(18)	28(8)	52(8)	-9(19)	60(19)	-4(12)
C(4)	6069(12)	3934(9)	6090(8)	73(17)	42(8)	28(6)	-9(20)	15(16)	-27(12)
N(1)	7362(10)	3888(7)	5370(7)	65(14)	27(6)	41(6)	-1(16)	30(14)	-13(10)
N(2)	6060(10)	5015(7)	6836(7)	67(14)	35(7)	48(6)	-11(16)	91(16)	-11(11)
N(3)	4869(11)	2987(8)	6121(7)	101(16)	40(7)	51(7)	-62(18)	71(17)	-22(12)

TABLE 2-b. FRACTIONAL COORDINATES OF HYDROGEN ATOMS ($\times 10^4$)

Atom	Bound to	x	y	z
H(1)	O(4)	9371	4211	3279
H(2)	C(1)	8986	556	3887
H(3)	C(1)	9596	1635	2605
H(4)	C(2)	10178	2399	5368
H(5)	C(3)	7328	1700	5079
H(6)	C(3)	6938	2960	3645
H(7)	N(1)	8501	4679	5425
H(8)	N(2)	5157	5227	7297
H(9)	N(2)	6953	5635	6917
H(10)	N(3)	4084	2982	6855
H(11)	N(3)	4764	2383	5455

standard deviations. The observed and calculated structure factors are listed in Table 3. Figure 1 shows bond distances and angles with the numbering of atoms. The bond lengths and angles are compared in Table 4 with those of other compounds such as L-arginine dihydrate,⁷⁾ taurine,^{8,9)} homotaurine,¹⁰⁾ GABA,¹¹⁾ GABOB,¹²⁾ and γ -guanidinobutyric acid hydrochloride (GGBA·HCl).¹³⁾ Similarly, in the cases of taurine and homotaurine, the guanidyl group is protonated by one hydrogen atom of the sulfonate group, the three S-O bonds of the resultant $-\text{SO}_3^-$ group being equivalent in the state of resonance. The average O-S-O and C-S-O angles in the sulfonate group are 112.1 and 106.7°, respectively. Deviations from the tetrahedral angles are probably due to the repulsion between the adjacent oxygen atoms which lie at the short contact distances of 2.42 Å as discussed in taurine by Sutherland and Young.⁸⁾

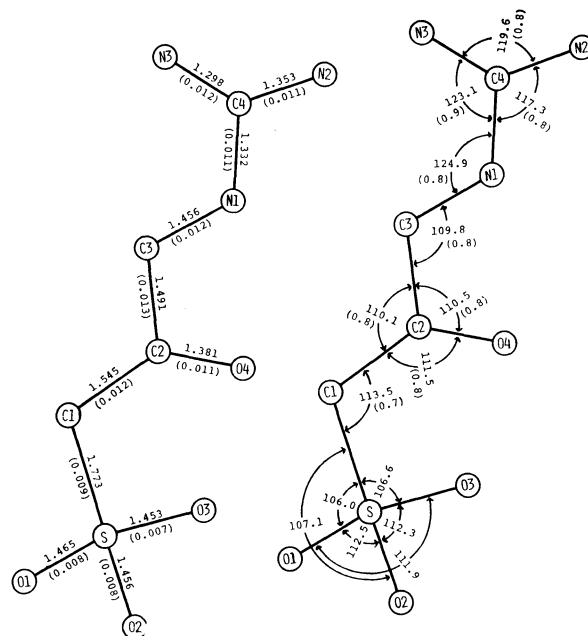


Fig. 1. Bond lengths (Å) and angles (°) of GGBOPSA. Estimated standard deviations are listed in the parentheses and those of angles around sulfur atom are 0.5°.

The guanidyl group is planar and the equation of the least-squares plane through the four atoms, N(1), C(4), N(2), and N(3), is

$$-0.51539X + 0.47909Y - 0.71053Z = -4.76419.$$

Deviations of the individual atoms from this plane are N(1): -0.0027, C(4): 0.0081, N(2): -0.0026 and N(3): -0.0028 Å. The dihedral angle between this plane and that passing through C(1)-C(2)-C(3) is 27.4°. In L-arginine dihydrate,⁷⁾ the deviations of the individual atoms from the least-squares plane of guanidyl group are N(1): -0.0005, C(4): 0.0015, N(2): -0.0005, and N(3): -0.0005 Å. Thus, the planarity of the guanidyl group in GGBOPSA is in good agreement with that of L-arginine dihydrate. All the C-N bond distances of the guanidyl group are halfway between the value of single bond (1.47 Å) and that of double bond (1.24 Å) proposed by Shomaker and

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- 8) H. H. Sutherland and D. W. Young, *ibid.*, **16**, 897 (1963).
- 9) Y. Okaya, *ibid.*, **21**, 726 (1966).
- 10) S. Ueoka, T. Fujiwara, and K. Tomita, *This Bulletin*, **45**, 3634 (1972).
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- 12) M. Harada, H. Higashi, T. Fujiwara, and K. Tomita, unpublished result.
- 13) T. Maeda, T. Fujiwara, and K. Tomita, *This Bulletin*, **45**, 3628 (1972).

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TABLE 4. COMPARISON OF BOND LENGTHS (Å) AND ANGLES (°) WITH RELATED COMPOUNDS

Length	GGBOPSA	Homota- urine	Taurine	L-Arginine	GGBA · HCl	GABA	GABOB
C (1)–C (2)	1.545	1.526	1.520	1.540	1.557	1.519	1.525
C (2)–C (3)	1.491	1.508	—	1.517	1.528	1.502	1.516
C (3)–N (1)	1.456	1.486	1.484	1.471	1.477	1.469	1.477
C (4)–N (1)	1.332	—	—	1.351	1.317	—	—
C (4)–N (2)	1.353	—	—	1.340	1.338	—	—
C (4)–N (3)	1.298	—	—	1.322	1.318	—	—
S–O (1)	1.465	1.445	1.461	—	—	—	—
S–O (2)	1.456	1.469	1.448	—	—	—	—
S–O (3)	1.453	1.469	1.465	—	—	—	—
S–C (1)	1.773	1.761	1.780	—	—	—	—
C (2)–O (4)	1.381	—	—	—	—	—	1.425
Angle							
O (1)–S–O (2)	112.5	112.5	113.7	—	—	—	—
O (1)–S–O (3)	111.9	112.5	110.9	—	—	—	—
O (2)–S–O (3)	112.3	110.7	113.0	—	—	—	—
C (1)–S–O (1)	106.0	107.3	105.8	—	—	—	—
C (1)–S–O (2)	107.1	106.7	106.9	—	—	—	—
C (1)–S–O (3)	106.6	106.7	105.8	—	—	—	—
S–C (1)–C (2)	113.5	112.0	112.9	—	—	—	—
C (1)–C (2)–C (3)	110.1	110.7	—	110.1	107.1	113.0	110.8
C (2)–C (3)–N (1)	109.5	109.8	112.6	111.1	107.8	111.8	109.5
C (3)–N (1)–C (4)	124.9	—	—	123.2	123.7	—	—
N (1)–C (4)–N (2)	117.3	—	—	121.0	120.9	—	—
N (1)–C (4)–N (3)	123.1	—	—	118.9	120.3	—	—
N (2)–C (4)–N (3)	119.6	—	—	120.2	118.7	—	—
C (1)–C (2)–O (4)	111.5	—	—	—	—	—	111.1
C (3)–C (2)–O (4)	110.5	—	—	—	—	—	107.0

Stevensen,¹⁴ the average being 1.328 Å. We see from Table 4 that C–N distances of the guanidyl group differ (greater than 2σ) from those of GGBA·HCl. This difference is probably due to the difference of molecular environments, *i.e.*, GGBOPSA molecule is in free state while GGBA molecule is in hydrochloride salt state. Three C–N bonds of GGBOPSA have somewhat double bond character and calculation by Pauling's method¹⁵ indicates that the double bond characters of C(4)–N(1), C(4)–N(2), and C(4)–N(3) bonds are 32, 25, and 43%, respectively, whereas the corresponding values for GGBA·HCl are 35, 29, and 36%.¹³

It is of interest to note that C(2)–O(4) distance of the hydroxyl group is 1.381 Å, significantly shorter

than that of found in GABOB (1.425 Å) which is normal C–O single bond. Other bond distances and angles in the molecule are quite normal.

The skeletal conformation of GGBOPSA molecule (Fig. 2) is of *trans* zigzag form as found in GGBA·HCl, GABA·HCl, GABOB, and homotaurine. The torsion angles around C(1)–C(2) and C(2)–C(3), which are in the skeletal conformation of the molecules, are both almost 180° in homotaurine, GABA·HCl, and GGBA·HCl. On the other hand, the corresponding values of GGBOPSA are 161.9 and 177.8°, and those of GABOB, 173.7 and 168.8°, respectively. The effect of β -hydroxyl group in the molecule might be one of the factors influencing the restricted conformation and

TABLE 5. HYDROGEN BOND LENGTHS (Å) AND ANGLES (°) OF GGBOPSA

Bond length (Å)		Bond angle (°)	
O (4)–H (1)–O (1) (I)	2.732	C (2)–O (4)–O (1) (I)	110.4
N (1)–H (7)–O (4) (II)	2.907	C (3)–N (1)–O (4) (II)	127.0
N (2)–H (8)–O (2) (II)	2.944	C (4)–N (2)–O (2) (II)	137.0
N (2)–H (8)–O (4) (II)	3.231	C (4)–N (2)–O (4) (II)	91.7
N (2)–H (9)–O (1) (III)	3.271	C (4)–N (2)–O (1) (III)	111.9
N (3)–H (10)–O (2) (III)	2.827	C (4)–N (3)–O (2) (III)	114.4
N (3)–H (11)–O (3) (IV)	2.945	C (4)–N (3)–O (3) (IV)	150.9
(I) (2.0– x , 0.5+ y , 0.5– z)		(II) (2.0– x , 1.0– y , 1.0– z)	
(III) (–1.0+ x , 0.5– y , 0.5+ z)		(IV) (–1.0+ x , y , z)	

14) V. Shomaker and D. P. Stevensen, *J. Amer. Chem. Soc.*, **63**, 37 (1941).

15) L. Pauling, "The Nature of the Chemical Bond," 3rd. ed., Cornell University Press, Ithaca (1960), p. 232.

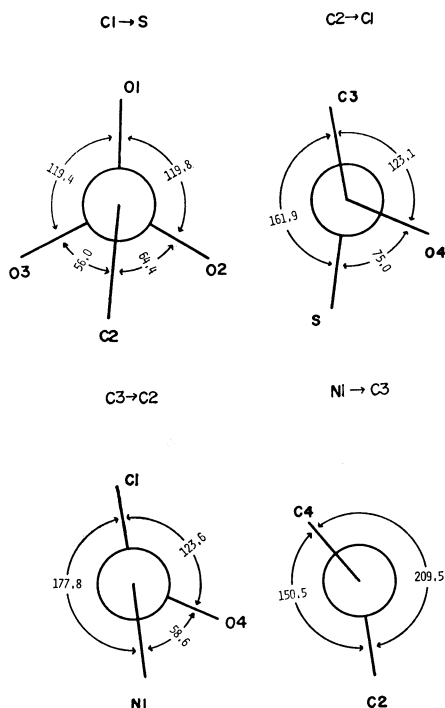


Fig. 2. Newman projection of atoms around four bonds. The arrow indicates the bond direction viewing down from front to back of paper.

also the physiological action. Torsion angles of sulfonate group have similar values to those of homotaurine. The torsion angle around C(3)–N(1) is 150.5° , which is similar to 162.0° of L-arginine dihydrate⁷⁾ calculated.

Similarly in the case of L-arginine dihydrate, GG-BOPSA molecule occurs in zwitterionic form, $(\text{NH}_2)_2^+ \text{CNHCH}_2\text{CH}(\text{OH})\text{CH}_2\text{SO}_3^-$.

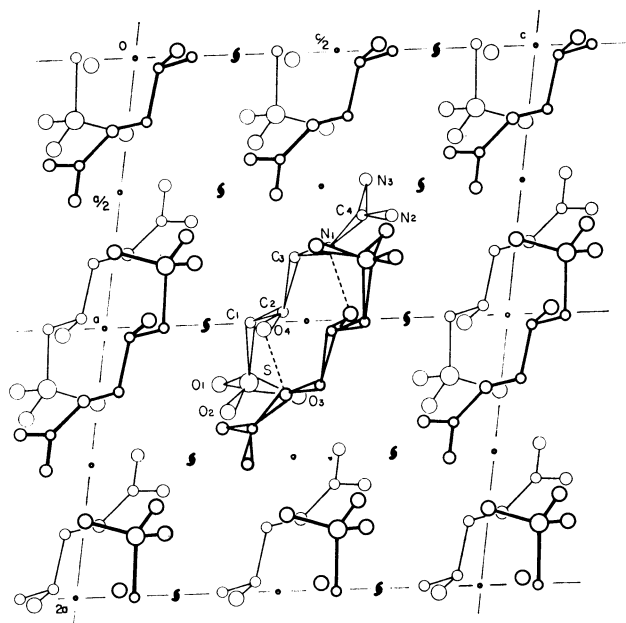


Fig. 3. The crystal structure projected along *b*-axis.

Distances and angles of hydrogen bonds are listed in Table 5. As shown in Fig. 3, *d*- and *l*-forms of GG-BOPSA molecules were dimerized through the N(1)–H...O(4) hydrogen bonds ($2.907 \text{ \AA}$) related by a center of symmetry. This cyclic *d*-*l* dimerization can be also seen in GABOB,¹²⁾ which were dimerized through OH...O hydrogen bond between β -OH group and oxygen atom of carboxyl group related by a center of symmetry. In these cases, however, the oxygen atom, O(4), of β -hydroxyl group of GG-BOPSA molecule takes part in the intermolecular hydrogen bond system as an acceptor, while β -OH of GABOB is used to form intra- and intermolecular bifurcated hydrogen

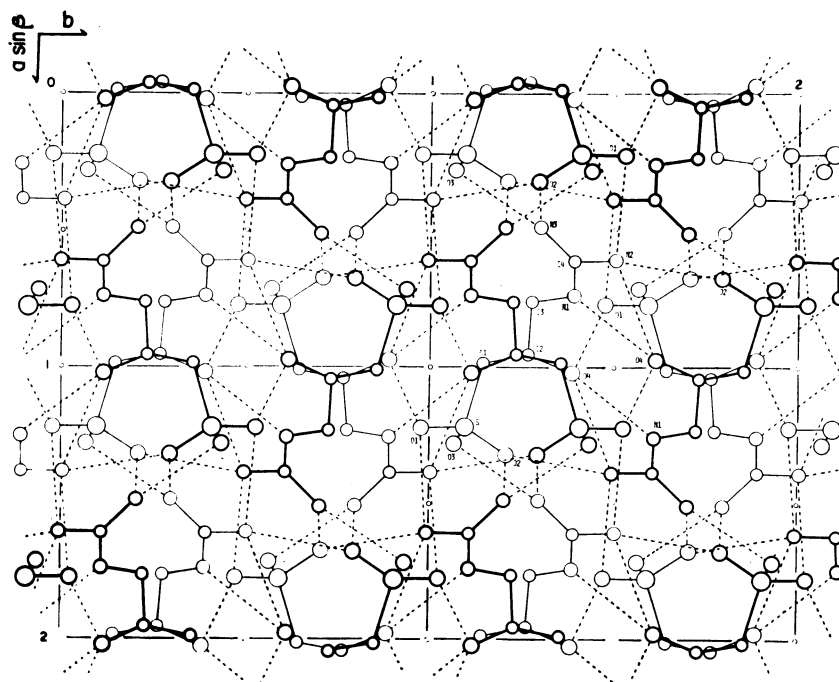


Fig. 4. The crystal structure projected along *c*-axis. The broken lines indicate the hydrogen bonds.

bond as a donor.

The crystal structure projected downward to c -axis is shown in Fig. 4. Among the hydrogen atoms in the molecule, all the feasible ones are utilized to form hydrogen bonds and the molecules are held together by three-dimensional network of $\text{NH}\cdots\text{O}$ and $\text{OH}\cdots\text{O}$ hydrogen bonds. The guanidyl group is connected with three neighboring molecules by six hydrogen bonds, the sulfonate group acting as an acceptor of five hydrogen bonds, and oxygen atom of hydroxyl group as both acceptor and donor. The distances of $\text{N}(2)$ to $\text{O}(2)$ and to $\text{O}(4)$ by a translational operation ($2.0-x, 1.0-y, 1.0-z$) are 2.994 and 3.231 Å, respectively,

$\text{H}(8)$ atom being located on a line bisecting these two directions. Thus, the $\text{H}(8)$ atom seems to contribute to form a bifurcated hydrogen bond. On the other hand, homotaurine molecules are jointed with each other with three $\text{NH}\cdots\text{O}$ hydrogen bonds to form a three-dimensional network, while in taurine, there are three $\text{NH}\cdots\text{O}$ intermolecular hydrogen bonds and one intramolecular hydrogen bonding. The intermolecular contacts between adjacent molecules are kept by normal van der Waals distances.

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