

so. No definite trends can be seen yet for the Schiff's base grouping since the angle values from the present work differ substantially from the previous work (Bürgi & Dunitz, 1970).

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## The Structure of the Tripeptide L-Alanyl-L-alanyl-L-alanine

BY J. KEITH FAWCETT AND NORMAN CAMERMAN

*Biochemistry Department, University of Toronto, Toronto, Ontario, Canada*

AND ARTHUR CAMERMAN

*Departments of Medicine (Neurology) and Pharmacology, University of Washington, Seattle, Washington 98195, U.S.A.*

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The tripeptide L-alanyl-L-alanyl-L-alanine, a competitive inhibitor of the enzyme elastase, crystallizes from a water/dimethylformamide solution as a hemihydrate ( $C_9H_{17}N_3O_4 \cdot \frac{1}{2}H_2O$ ). The unit-cell parameters are  $a = 18.513$  (8),  $b = 5.330$  (3),  $c = 24.775$  (10) Å,  $\beta = 98.64$  (4)°. The space group is  $C2$  with  $Z = 8$  (two molecules per asymmetric unit). The data were collected on a four-circle diffractometer and the structure was solved by direct methods and refined to  $R = 0.031$ . The tri-L-alanine molecules are packed in an anti-parallel pleated-sheet arrangement. Precise molecular and conformational parameters are given.

### Introduction

The tripeptide L-alanyl-L-alanyl-L-alanine (AAA) has been found to be an effective competitive inhibitor of the esterolytic activity of the pancreatic enzyme elastase (Dzialoszynski & Hofmann, 1973). Shotton, White & Watson (1971) have studied the crystal structure of the tri-L-alanine-elastase complex at 3.5 Å

resolution. Their difference electron-density map shows firstly that tri-L-alanine binds with almost full occupancy near the catalytic site of elastase and, secondly, that there are no secondary binding sites. In this paper we present precise molecular and conformational parameters for tri-L-alanine which may be of use in interpreting substrate-enzyme interactions for the tri-L-alanine-elastase complex as well as furnishing

detailed conformational characteristics for studying peptide structure.

### Experimental

Crystals of L-alanyl-L-alanyl-L-alanine hemihydrate, obtained by slow evaporation of a water/dimethylformamide solution, are colourless needles elongated along **b**. The unit-cell parameters were determined by measurement of various axial reflections on a four-circle goniometer.

#### Crystal data

[ $\lambda(\text{Cu } K\alpha) = 1.54178$ ,  $\lambda(\text{Cu } K\alpha_1) = 1.54051$ ,  $\lambda(\text{Cu } K\alpha_2) = 1.54433$  Å.] L-Alanyl-L-alanyl-L-alanine hemihydrate  $\text{C}_9\text{H}_{17}\text{N}_3\text{O}_4 \cdot \frac{1}{2}\text{H}_2\text{O}$ , M. W. 240.3. Monoclinic,  $a = 18.513$  (8),  $b = 5.330$  (3),  $c = 24.775$  (10) Å,  $\beta = 98.64$  (4)° (errors are  $2\sigma$ ).  $U = 2416.9 \pm 3.5$  Å<sup>3</sup>.  $D_m$  (floatation in nitrobenzene/bromobenzene)  $\approx 1.28$  g cm<sup>-3</sup>;  $Z = 8$ ,  $D_x = 1.32$  g cm<sup>-3</sup>. Absorption coefficient for Cu  $K\alpha$  X-rays:  $\mu = 9.1$  cm<sup>-1</sup>.  $F(000) = 1032$ . Absent spectra:  $hkl$  when  $h+k$  odd. Space group  $C2$  (confirmed by structure analysis) with two molecules per asymmetric unit.

The intensities of all reflections with  $2\theta(\text{Cu } K\alpha) \leq 130^\circ$  (corresponding to a minimum interplanar spacing  $d = 0.85$  Å) were measured on an automated four-circle diffractometer with nickel-filtered Cu  $K\alpha$  radiation using the  $2\theta$ - $\theta$  scan technique. The intensities were corrected for background and Lorentz and polarization factors were applied. The crystal used for recording the intensities had cross-section  $0.12 \times 0.04$  mm; absorption was low and no corrections were applied. A total of 2298 unique reflections were measured, and of these 2177 (95%) had  $I > 2\sigma(I)$  and were considered to be observed.

#### Structure determination

Because of the short **b** axis, it was assumed from the beginning that the length of the peptide chains would lie perpendicular to **b**. Thus, initial attempts were made to determine the structure by direct phasing methods in two dimensions using the centrosymmetric  $h0l$  data. A number of solutions produced promising electron-density distributions but in no case could tentative atomic positions be refined.

The structure was solved by the multiple-solution tangent formula program (*MULTAN*) of Germain, Main & Woolfson (1971). The starting set of reflections was produced by the *CONVERGE* section of *MULTAN*. The origin was specified by assigning a phase value of 0 to the 110 reflection and  $\pi/4$  to the  $0,2,21$  reflection which also fixed the enantiomorph. The phase of the  $40\bar{2}$  reflection was determined by the  $\sum_1$  relationship. Phases of reflections  $2,0,2\bar{2}$  and  $12,0,1\bar{2}$  were allowed to take values of 0 or  $\pi$ , and reflection 111 was given starting values of  $\pm\pi/4$ ,  $\pm 3\pi/4$ , altogether producing 16 phase sets. These could be grouped ac-

ording to the values of their various figures of merit (Germain *et al.*, 1971), and the five resulting groups are given in Table 1. Various criteria useful for choosing the 'best' set of phases are shown: the absolute figure of merit and  $\sum\alpha_h$  are related to the internal consistency of the set of phases and should be a maximum for the 'correct' phase set;  $R_{\text{Karle}}$  (Karle & Karle, 1966) should be a minimum. The fourth figure of merit,  $\psi_0 = \sum_h |\sum_{h'} E_{h'} E_{h-h'}|$  is of particular value in

space groups such as  $C2$  which lack translational symmetry. The terms in the inner summation are those for which phases have been calculated, and those in the outer summation are computations for a number (50 in our case) of reflections having very small  $E$ 's. For the correct solution those  $E$ 's which are observed to have small values should also calculate small and therefore the overall sum should be a minimum for the correct phase set. Table 1 shows that  $\psi_0$  and  $R_{\text{Karle}}$  were the most reliable indicators, for set *A* gave a clearly interpretable  $E$  map containing all non-hydrogen atoms (and most of the hydrogen positions!) despite having the second lowest value of both absolute figure of merit and  $\sum\alpha_h$ . The  $E$  map also revealed the presence of two water molecules, each situated on a twofold axis. For set *A*, phases of all 64 of the  $h0l$  structure invariants with  $E \geq 1.5$  were determined correctly as confirmed by the final calculated phase angles. Group *E* represents trivial phase sets with all  $h0l$  phase angles equal to 0. It is interesting to note that an earlier *MULTAN* run in which *CONVERGE* selected the 400 reflection in place of the  $12,0,1\bar{2}$  failed to give the correct solution (we subsequently deleted the 400 reflection from the input  $E$ 's for further trials).

Table 1. Groups of phase sets with their figures of merit

Group	Number of sets in group	$\sum\alpha_h$ ( $\times 10^{-4}$ )	Absolute figure of merit	$R_{\text{Karle}}$	$\psi_0^*$ ( $\times 10^{-3}$ )	†
<i>A</i>	1	1.17	1.06	25.9	1.83	100
<i>B</i>	1	1.10	0.98	32.7	1.82	72
<i>C</i>	4	1.18	1.08	29.1	2.02	47
<i>D</i>	7	1.26	1.18	27.5	2.19	44
<i>E</i>	3	1.46	1.42	21.2	2.64	63

\*  $\psi_0 = \sum_h |\sum_{h'} E_{h'} E_{h-h'}|$ .

† Percentage of  $h0l$  structure invariants with correct signs.

Three cycles of full-matrix isotropic least-squares refinement for the non-hydrogen atoms gave  $R = 0.129$  for all reflections. One anisotropic cycle gave  $R = 0.075$  and a subsequent difference Fourier map clearly showed all hydrogen positions ( $\rho = 0.2-0.4$  e Å<sup>-3</sup>). Two cycles of full anisotropic refinement of the non-hydrogen ('heavy') atoms followed by a cycle of refinement of the hydrogen positions produced  $R = 0.037$ . Anomalous dispersion corrections (Cromer & Liberman, 1970) were applied to the heavy atoms, and two anisotropic cycles of refinement of the heavy atoms and one more of the hydrogen positions gave a final  $R = 0.033$  for all

Table 2. *Final positional and thermal parameters for the non-hydrogen atoms*Values are  $\times 10^5$ . Standard deviations are given in parentheses.  $T = \exp[-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl)]$ .

Molecule <i>A</i>	<i>x</i>	<i>y</i>	<i>z</i>	$\beta_{11}$	$\beta_{22}$	$\beta_{33}$	$\beta_{12}$	$\beta_{13}$	$\beta_{23}$
N(1)	7200 (11)	4500*	57046 (8)	189 (6)	3024 (106)	68 (3)	83 (24)	18 (4)	40 (17)
C(1 <i>A</i> )	12041 (13)	8061 (77)	62326 (9)	141 (7)	2672 (114)	63 (4)	41 (25)	15 (4)	42 (19)
C(1 <i>B</i> )	13926 (19)	35673 (85)	62940 (12)	388 (12)	3184 (147)	125 (5)	-288 (37)	71 (7)	-41 (25)
C(1)	8107 (12)	-134 (73)	66997 (9)	163 (7)	2414 (112)	62 (4)	102 (26)	23 (4)	23 (18)
O(1)	1436 (9)	1689 (73)	66650 (7)	151 (5)	6073 (133)	99 (3)	201 (24)	29 (3)	316 (19)
N(2)	12391 (10)	-7980 (67)	71461 (7)	131 (5)	2628 (95)	55 (3)	108 (21)	19 (3)	37 (15)
C(2 <i>A</i> )	9523 (13)	-14650 (76)	76432 (9)	143 (7)	2685 (116)	62 (4)	57 (25)	19 (4)	55 (19)
C(2 <i>B</i> )	7757 (19)	-42397 (87)	76578 (12)	417 (13)	3187 (146)	106 (5)	-288 (39)	22 (6)	68 (24)
C(2)	15138 (12)	-7347 (73)	81330 (9)	152 (7)	2416 (109)	62 (4)	87 (25)	14 (4)	24 (18)
O(2)	21731 (9)	-9668 (73)	81183 (7)	132 (5)	6089 (132)	92 (3)	227 (23)	19 (3)	-191 (18)
N(3)	12425 (10)	487 (72)	85651 (7)	119 (6)	3372 (106)	64 (3)	63 (23)	20 (3)	-56 (17)
C(3 <i>A</i> )	16741 (14)	7149 (79)	90858 (10)	157 (7)	3095 (126)	66 (4)	115 (27)	13 (4)	-63 (20)
C(3 <i>B</i> )	18681 (19)	34808 (89)	91048 (13)	355 (12)	3704 (159)	140 (6)	-273 (39)	-7 (6)	-98 (27)
C(3)	12506 (14)	469 (80)	95501 (9)	206 (8)	3108 (128)	73 (4)	278 (30)	39 (4)	39 (20)
O(3)	5940 (9)	-5917 (70)	94259 (7)	192 (6)	5087 (122)	108 (3)	121 (24)	43 (3)	268 (18)
O(4)	15830 (10)	2508 (76)	100224 (7)	278 (7)	6159 (137)	62 (3)	327 (28)	19 (3)	-66 (18)
Molecule <i>B</i>									
N(1)	7408 (10)	23366 (61)	6936 (7)	172 (6)	2221 (87)	50 (3)	12 (22)	12 (3)	-6 (15)
C(1 <i>A</i> )	12397 (13)	32582 (71)	11801 (9)	147 (7)	1937 (98)	57 (4)	-12 (23)	6 (4)	33 (17)
C(1 <i>B</i> )	12691 (17)	61026 (78)	11795 (11)	308 (11)	2289 (119)	86 (4)	-152 (31)	-7 (6)	27 (21)
C(1)	9664 (12)	22615 (70)	16885 (9)	146 (7)	1599 (91)	63 (4)	27 (24)	15 (4)	-29 (17)
O(1)	3339 (9)	14899 (65)	16617 (6)	148 (5)	4188 (104)	76 (3)	-246 (20)	11 (3)	15 (15)
N(2)	14316 (10)	22873 (66)	21502 (7)	121 (5)	2415 (91)	58 (3)	-107 (21)	17 (3)	25 (15)
C(2 <i>A</i> )	12120 (13)	13323 (73)	26522 (9)	148 (7)	1943 (99)	59 (4)	-29 (24)	19 (4)	22 (17)
C(2 <i>B</i> )	12689 (18)	-15012 (81)	26802 (11)	382 (12)	2224 (122)	95 (5)	-76 (33)	19 (6)	40 (21)
C(2)	16782 (12)	25026 (72)	31448 (9)	149 (7)	1883 (99)	61 (4)	-14 (24)	10 (4)	73 (18)
O(2)	23232 (9)	30549 (66)	31377 (6)	145 (5)	4251 (101)	80 (3)	-194 (20)	25 (3)	-33 (15)
N(3)	13481 (10)	27583 (68)	35826 (7)	142 (6)	2941 (106)	58 (3)	-180 (23)	23 (3)	-42 (16)
C(3 <i>A</i> )	17220 (14)	35796 (80)	41160 (10)	162 (7)	3148 (129)	67 (4)	-130 (27)	13 (4)	-44 (20)
C(3 <i>B</i> )	18198 (19)	64035 (88)	41455 (12)	357 (12)	3432 (151)	121 (5)	-360 (37)	22 (6)	-86 (25)
C(3)	12668 (14)	27663 (84)	45473 (10)	235 (9)	3595 (144)	79 (4)	-210 (32)	36 (5)	-105 (22)
O(3)	5869 (10)	29956 (80)	44188 (8)	206 (6)	6580 (148)	137 (4)	-404 (28)	60 (4)	-219 (22)
O(4)	15818 (12)	20874 (87)	49948 (8)	345 (8)	9150 (206)	92 (3)	-69 (37)	35 (4)	344 (24)
O( <i>W</i> 1)	0	59845 (73)	0	254 (8)	1937 (106)	102 (4)	0	-1 (5)	0
O( <i>W</i> 2)	0	66007 (91)	50000	393 (12)	3291 (160)	311 (9)	0	116 (8)	0

\* Position held constant to fix origin along *b*.Table 3. *Final positional parameters for hydrogen atoms*Values are  $\times 10^4$ . Standard deviations are given in parentheses.

	Molecule <i>A</i>			Molecule <i>B</i>		
	<i>x</i>	<i>y</i>	<i>z</i>	<i>x</i>	<i>y</i>	<i>z</i>
H(11)	280 (14)	1504 (64)	5691 (10)	346 (14)	1497 (60)	816 (9)
H(12)	975 (14)	1142 (65)	5407 (10)	985 (14)	1596 (60)	470 (10)
H(13)	605 (15)	-1089 (70)	5640 (11)	518 (14)	3721 (63)	501 (10)
H(1 <i>A</i> )	1647 (14)	-288 (64)	6232 (10)	1726 (13)	2537 (60)	1164 (9)
H(1 <i>B</i> 1)	952 (17)	4636 (72)	6293 (11)	800 (16)	6647 (65)	1208 (11)
H(1 <i>B</i> 2)	1599 (17)	4142 (69)	5974 (12)	1404 (15)	6817 (62)	830 (11)
H(1 <i>B</i> 3)	1739 (17)	4048 (71)	6630 (12)	1610 (15)	6648 (63)	1497 (11)
H(2)	1668 (13)	-1042 (61)	7159 (9)	1855 (13)	2762 (61)	2165 (9)
H(2 <i>A</i> )	523 (14)	-579 (60)	7653 (10)	699 (13)	1876 (58)	2648 (9)
H(2 <i>B</i> 1)	419 (17)	-4641 (73)	7318 (11)	987 (16)	-2339 (66)	2355 (11)
H(2 <i>B</i> 2)	585 (16)	-4593 (73)	8004 (12)	1125 (16)	-2134 (66)	3020 (11)
H(2 <i>B</i> 3)	1201 (18)	-5067 (75)	7698 (12)	1790 (17)	-1981 (66)	2703 (11)
H(3)	778 (13)	140 (66)	8548 (9)	891 (13)	2270 (65)	3562 (9)
H(3 <i>A</i> )	2096 (14)	-380 (64)	9130 (10)	2191 (14)	2590 (66)	4205 (10)
H(3 <i>B</i> 1)	1418 (17)	4497 (74)	9086 (12)	1346 (17)	7319 (75)	4107 (11)
H(3 <i>B</i> 2)	2138 (16)	4036 (70)	8768 (12)	2095 (16)	6915 (72)	3824 (12)
H(3 <i>B</i> 3)	2196 (16)	3901 (72)	9449 (12)	2103 (16)	7097 (74)	4522 (11)
H( <i>W</i> )	-265 (14)	7142 (63)	185 (10)	-221 (18)	5452 (81)	5259 (13)

reflections and  $R=0.031$  for the observed reflections.\* A difference Fourier synthesis at this stage showed no

\* The table of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 30722 (20 pp., 1 microfiche). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

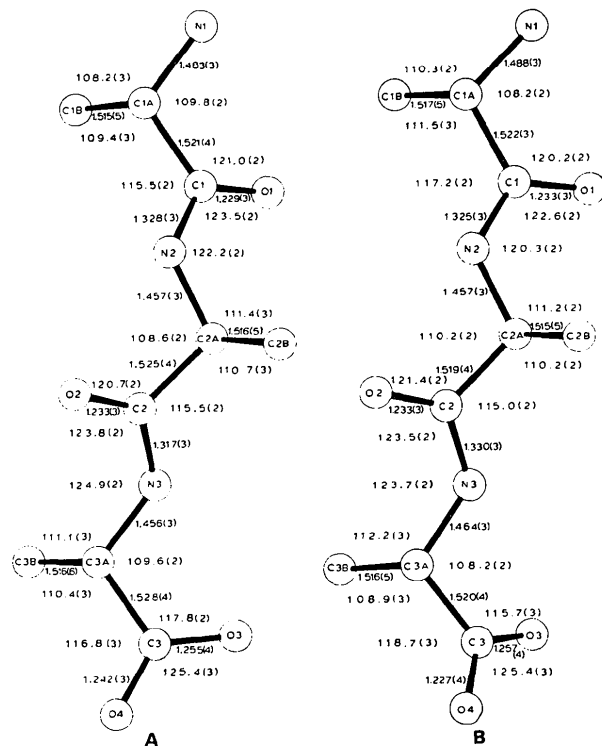


Fig. 1. Bond lengths ( $\text{\AA}$ ) and valency angles ( $^\circ$ ) for crystallographically independent molecules *A* and *B*. Standard deviations are in parentheses. Also shown are the numbering scheme and the conformations of the two molecules.

residual density above  $0.1 \text{ e \AA}^{-3}$ . The maximum shift/error in parameters for the final cycle was 0.1 for the heavy atoms and 0.5 for the hydrogen positions. Throughout the refinement, hydrogen temperature factors were set equal to those of the atoms to which the hydrogens were attached. Unit weights were used; the final  $\sum w(F_o - F_c)^2 / (m - n) = 0.94$ . The scattering factors of the heavy atoms were those of Cromer & Mann (1968) and for the hydrogen atoms those of Stewart, Davidson & Simpson (1965).

Table 2 contains the final positional and thermal parameters of the nonhydrogen atoms and Table 3 the positional parameters of the hydrogen atoms.

## Discussion

Fig. 1 shows the individual interatomic bond lengths and valency angles for the non-hydrogen atoms. Bond lengths and angles averaged over all chemically equivalent bonds within both of the crystallographically independent molecules are given in Table 4 and compared to the same distances in di-L-alanine (Fletcher, Tsai & Hughes, 1971) and di-L-alanine hydrochloride (Tokuma, Ashida & Kakudo, 1969). Our averaged value of  $1.325 \text{ \AA}$  for the peptide bond [C-N(peptide)] is significantly shorter than the values reported for di-L-alanine and di-L-alanine.HCl (1.344 and  $1.35 \text{ \AA}$ ), but agrees well with the weighted averages for amino acid structures calculated by Corey & Pauling (1953) and Marsh & Donohue (1967). The average peptide bond length is in satisfactory agreement also with neutron-diffraction values of  $1.326(3) \text{ \AA}$  for  $\alpha$ -glycylglycine (Freeman, Paul & Sabine, 1970) and  $1.330(3) \text{ \AA}$  for glycylglycine.HCl.H<sub>2</sub>O (Koetzle, Hamilton & Parthasarathy, 1972). Because the C(A)-C(B) (methyl) bond lengths seemed short we calculated corrections due to thermal libration. Using the method of Schomaker & Trueblood (1968) we

Table 4. Averaged bond lengths ( $\text{\AA}$ ) and valency angles ( $^\circ$ )

Number of contributors	Bond	AAA*	AA <sup>1</sup>	AA <sup>2</sup> HCl	Weighted average <sup>3</sup>	Weighted average <sup>4</sup>
2	N(terminal)-C(A)	1.485 (2)	1.494	1.51	-	-
4	N(peptide)-C(A)	1.458 (2)	1.457	1.45	1.47	1.455
6	C(A)-C	1.522 (1)	1.535	1.53	1.53	1.51
4	C-O(carbonyl)	1.232 (1)†	1.226	1.21	1.24	1.24
4	C-N(peptide)	1.325 (3)	1.344	1.35	1.32	1.325
6	C(A)-C(B)	1.516 (1)†	1.521	1.55	-	-
2	C-O(3) (carboxyl)	1.256 (1)	1.241	1.27	-	-
2	C-O(4) (carboxyl)	1.242, 1.227†	1.228	1.17	-	-
Angle						
4	C-N-C(A)	122.8 (10)	122.9	121	123	122
4	N-C-C(A)	115.8 (5)	113.2	113	114	116
4	N-C-O	123.3 (3)	125.9	124	125	123.5
4	C(A)-C-O	120.8 (3)	120.9	123	121	120.5
6	C-C(A)-N	109.1 (4)	108.8	108	110	111
6	C-C(A)-C(B)	110.2 (4)	110.8	110	-	-
2	N(terminal)-C(A)-C(B)	109.3 (10)	107.4	108	-	-
4	N(peptide)-C(A)-C(B)	111.5 (3)	110.1	111	-	-

\* Figures in parentheses are r.m.s. deviations.

† Uncorrected for thermal motion. See text for corrected values. (1) Fletcher *et al.* (1971). (2) Tokuma *et al.* (1969). (3) Corey & Pauling (1953). (4) Marsh & Donohue (1967).

analyzed the thermal motion of the 16 heavy atoms in each of the AAA molecules in terms of rigid-body vibrations; in no case did the corrections to the bond lengths exceed one e.s.d. However, riding-motion corrections (Busing & Levy, 1964) produced significant ( $4-8\sigma$ ) corrections to the individual C(A)-C(B) and C-O bond lengths. The averaged bond lengths after correction for riding motion are C(A)-C(B), 1.534 (2), C-O(carbonyl), 1.254 (2), and C-O(carboxyl), 1.272 (3) Å. It is interesting to note that after correction all four C-O(carboxyl) bonds are within  $3\sigma$  of one another.

Most probably owing to the requirements of intermolecular hydrogen bonding, more individual variation occurs between chemically equivalent angles (Table 4) than between the bond lengths. The averages, however, agree well with those of Corey & Pauling (1953) and Marsh & Donohue (1967). A table giving the bond lengths and valency angles involving hydrogen atoms has been deposited with the table of structure factors.\*

In order to compare the conformations of the two crystallographically independent molecules the coordinates of the non-hydrogen atoms of molecule B were fitted by a least-squares procedure to those of molecule A, with a program written by S. C. Nyburg, Depart-

ment of Chemistry, University of Toronto. Except for the oxygen atoms of the terminal carboxylic acid group all atoms of molecule B were  $\leq 0.3$  Å from their counterparts in molecule A. The two molecules are shown side-by-side in Fig. 1 and the only noticeable conformational difference is seen to be at the carboxyl

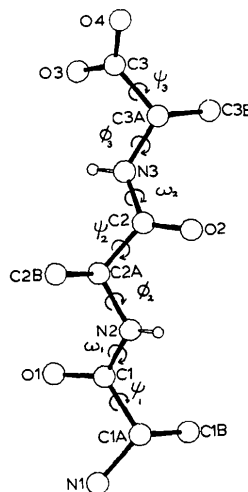


Fig. 2. Nomenclature for conformational angles in tri-L-alanine.

Table 5. Conformational angles ( $^{\circ}$ )

Standard deviations for tri-L-alanine are approximately  $0.3^{\circ}$ .

Bond Angle	N-C $_{\alpha}$		C $_{\alpha}$ -C			C-N	
	$\varphi_2$	$\varphi_3$	$\psi_1$	$\psi_2$	$\psi_3$	$\omega_1$	$\omega_2$
Tri-L-alanine. Molecule A	-145.7	-147.0	152.7	145.5	172.3	175.2	176.6
Molecule B	-156.2	-159.9	162.2	149.9	143.9	-179.2	173.0
Di-L-alanine (Fletcher <i>et al.</i> , 1971)	-113	-	165	103	-	176	-
Di-L-alanine.HCl (Tokuma <i>et al.</i> , 1969)	-153	-	157	163	-	-179	-
$\beta$ -Poly-L-alanine (Arnott <i>et al.</i> , 1967)	-139	-	135	-	-	-178	-
Anti-parallel pleated sheet (Miyazawa, 1961)	-142	-	145	-	-	180	-

Table 6. Lengths (Å) and angles ( $^{\circ}$ ) for hydrogen bonds

Donor-H...Acceptor	D...A ( $\sigma \sim 0.003$ Å)	H...A ( $\sigma \sim 0.03$ Å)	D-H...A angle ( $\sigma \sim 2.5^{\circ}$ )	Position of acceptor
Donor: peptide nitrogen				
N(2A)-H...O(2B)	2.918	2.16	158	( $\frac{1}{2}-x, -\frac{1}{2}+y, 1-z$ )
N(2B)-H...O(2A)	2.915	2.14	158	( $\frac{1}{2}-x, -\frac{1}{2}+y, 1-z$ )
N(3A)-H...O(1B)	2.988	2.17	160	( $-x, y, 1-z$ )
N(3B)-H...O(1A)	3.066	2.21	162	( $-x, y, 1-z$ )
Donor: -NH $_3^+$ nitrogen				
N(1A)-H...O(3B)	2.751	1.77	170	( $-x, y, -z$ )
N(1B)-H...O(3A)	2.900	2.08	145	( $-x, y, 1-z$ )
N(1A)-H...O(4B)	2.691	1.70	167	( $x, y, z$ )
N(1B)-H...O(4A)	2.685	1.83	174	( $x, y, -1+z$ )
N(1A)-H...O(W2)	2.887	2.18	140	( $x, -1+y, z$ )
N(1B)-H...O(W1)	2.812	1.89	168	( $x, y, z$ )
Donor: water				
O(W1)-H...O(3A)	2.652	1.71	170	( $x, 1+y, -1+z$ )
O(W2)-H...O(3B)	2.723	1.72	167	( $x, y, z$ )

\* See previous footnote.

terminal. The difference is attributable to the requirements of hydrogen bonding involving the terminal oxygen atoms. Table 5 gives the values of the conformational angles (Fig. 2) along the peptide chain in standard nomenclature (IUPAC-IUB Commission on Biochemical Nomenclature, 1971). The principal difference in conformation between molecules *A* and *B* is reflected in the two values for  $\psi_3$ . To facilitate conformational comparison with di-L-alanine and di-L-alanine hydrochloride we recalculated the torsion angles for those to conform with standard nomenclature. Perhaps surprisingly, the conformation of tri-L-alanine more closely resembles that of di-L-alanine hydrochloride

than di-L-alanine (Table 5); the effect of the chloride ion on the molecular conformation of di-L-alanine appears to be similar to the effects of the water molecules in tri-L-alanine.

The hydrogen atoms on all methyl groups and on N(1) of molecule *A* are in the staggered conformation with respect to the substituents on the  $\alpha$  carbon atoms. However, hydrogen-bonding forces result in the hydrogen atoms on N(1) in molecule *B* being close to the eclipsed conformation with respect to the substituents on C(1*A*), the torsion angles being 5.8, 10.0, 4.3°.

Fig. 3 shows a stereo view of the structure, viewed along the *b* axis. The tri-L-alanine molecules are packed

Table 7. Atomic displacements (Å) from least-squares planes

Molecule	<i>A</i>			<i>B</i>		<i>A</i>	<i>B</i>
Peptide unit	<i>i</i> =1	2	1	2		Carboxylic acid	
Number of plane	1	2	3	4		5	6
Displacements ( $\times 10^3$ )							
$C_{\alpha}^i$	-5	-4	-1	-5	$C_{\alpha}^j$	-3	-6
$C^i$	+17	+12	+3	+16	$C_{\alpha}^j$	+10	+21
$O^i$	-6	-5	-1	-6	O(3)	-4	-7
$N^{i+1}$	-6	-4	-1	-5	O(4)	-4	-8
$C_{\alpha}^{i+1*}$	-91	-64	+20	-140	$N^{3*}$	+201	+845
$H(N^{i+1})^*$	+81	-4	+24	-19			
Coefficients ( $\times 10^5$ )							
<i>a</i>	-2977	7055	34008	-24856		29876	1787
<i>b</i>	-93238	93732	-91901	91562		-95366	-93915
<i>c</i>	-36024	-34125	-19940	-31600		-3587	-34306
<i>d</i>	589269	-719358	-154049	-171038		-124327	-521518

$$\text{Equation of plane: } aX + bY + cZ + d = 0$$

\* These atoms were not included in the calculation of the plane.

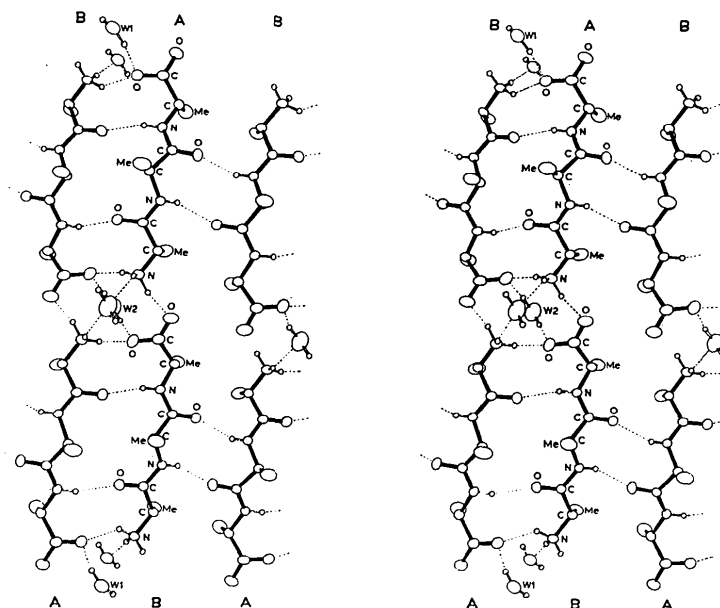


Fig. 3. Tri-L-alanine, a stereo view of the structure with *b* pointing away from the viewer. *c* points upward and *a* to the right. The oxygen atoms of *W*(1) at the bottom of the figure lie on the twofold axis at 0, *y*, 0; those on *W*(1) at the top are at 0, *y*, 1.

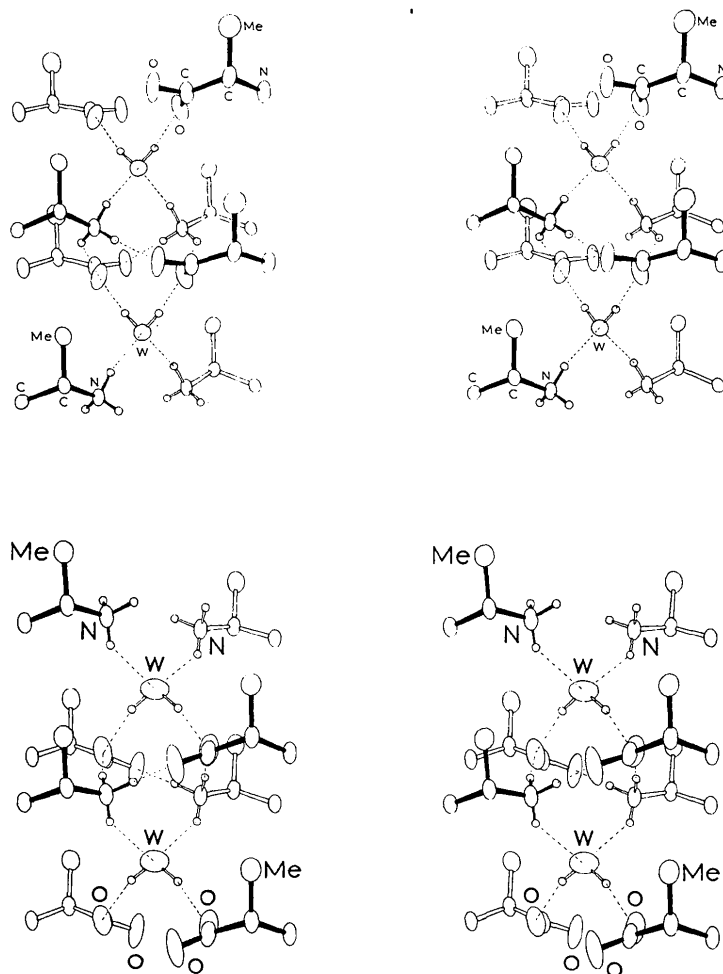


Fig. 4. Coordination around the water molecules,  $W(1)$  at top,  $W(2)$  at bottom. For both stereo pairs  $a$  points away from the viewer,  $c$  points right, and  $b$  points upward. The distance between the water molecules represents one translation along  $b$ .

in rows in head-to-tail fashion (C-terminal opposite N-terminal) with the methyl groups alternately above and below the planes through the peptide chains, and are held together in sheets by hydrogen bonds between all carbonyl oxygen and N-H groups of neighbouring molecules; this corresponds to the antiparallel pleated-sheet arrangement for polypeptide chains (Pauling & Corey, 1953). This arrangement lessens the steric hindrance between side chains which would occur for fully extended ( $\varphi = \psi = \omega = 180^\circ$ ) polypeptide chains. Tri-L-alanine provides the first precise and direct experimental measurements of the conformational angles (Table 5) for an antiparallel pleated-sheet arrangement. Previous values for the conformational angles have been derived from fiber diffraction studies of  $\beta$ -poly-L-alanine by Arnott, Dover & Elliott (1967) and calculated by Miyazawa (1961); these values are given in Table 5 for comparison with those of tri-L-alanine. The peptide chain repeat distances, measured from  $C_\alpha^1-C_\alpha^3$ , are 6.99 and 7.20 Å respectively for molecules  $A$  and  $B$ ,

compared with 6.9 Å in  $\beta$ -poly-L-alanine (Arnott *et al.* 1967).

As can be seen from the stereo view of Fig. 3 the bottom sheet of three molecules tilts downward with respect to the  $ac$  plane and the upper three tilt upward. The angle between these sheets is  $34^\circ$ . The general hydrogen-bonding scheme, in which all possible hydrogen donors take part, is also shown in Fig. 3. Hydrogen-bond parameters are given in Table 6. Marsh & Donohue (1967) have observed that hydrogen bonds involving the amide nitrogens as donors are significantly longer – and presumably weaker – than those involving the terminal  $-\text{NH}_3^+$  groups. Tri-L-alanine shows the same behaviour. The water molecules on the twofold axes fit neatly into the spaces between sheets and are vital in the intricate hydrogen-bonding network holding the terminal ends of the peptide molecules together (Fig. 4). Each water molecule cross-links four sheets. The water molecules have approximately tetrahedral environments. Excepting those distances

between atoms affected by hydrogen bonding, all other intermolecular contacts correspond to normal van der Waals interactions.

Deviations of atoms from the least-squares planes through the peptide and carboxylic acid groups are given in Table 7.

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## La Structure Cristalline de BaSrFe<sub>4</sub>O<sub>8</sub>

PAR D. HERMANN-RONZAUD

*Institut Laue-Langevin, B.P. 156, Centre de Tri, 38042-Grenoble Cedex, France*

ET M. BACMANN

*CNRS, Laboratoire des Rayons X, B.P. 166, Centre de Tri, 38042-Grenoble Cedex, France*

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BaSrFe<sub>4</sub>O<sub>8</sub> was prepared at 950°C. The structure has been studied by powder X-ray and neutron diffraction. The compound crystallizes in the trigonal space group  $P\bar{3}1m$ . The unit cell, with  $a = 5.450$  (2) and  $c = 8.101$  (3) Å, contains one molecule of BaSrFe<sub>4</sub>O<sub>8</sub>. The barium and strontium cations are octahedrally surrounded. The iron atoms are surrounded by oxygen tetrahedra as is aluminum in BaAl<sub>2</sub>O<sub>4</sub>, but the linkage of the tetrahedra is different. The atomic arrangement resembles that of feldspath BaAl<sub>2</sub>Si<sub>2</sub>O<sub>8</sub>. The structure was refined to  $R = 2.4\%$ . It disagrees with the structure proposed by Lucchini, Minichelli & Meriani [*Acta Cryst.* (1973). **B29**, 919–920] ( $R = 17\%$ ).

### Introduction

Lors d'une étude des ferrites mixtes d'alcalino-terreux, la structure cristalline de BaCaFe<sub>4</sub>O<sub>8</sub> a été établie (Herrmann & Bacmann, 1971) et le composé isomorphe BaSrFe<sub>4</sub>O<sub>8</sub> a été identifié. Il cristallise dans le groupe d'espace  $P\bar{3}1m$ , avec les paramètres de maille  $a = 5,450$  (2),  $c = 8,101$  (3) Å et une unité moléculaire par maille (Hermann, 1971). Cette phase, préparée à 950°C, se distingue de celle obtenue à plus haute température par Meriani & Slocari (1970) et décrite par

une maille orthorhombique:  $a = 5,516$ ,  $b = 8,265$  et  $c = 9,188$  Å.

Plus récemment, Lucchini, Minichelli & Meriani (1973) ont à leur tour mis en évidence la phase basse température hexagonale:  $a = 5,448$ ,  $c = 8,091$  Å. Ils en ont proposé la structure dans le groupe  $P\bar{6}m2$ , en désaccord avec nos résultats préliminaires.

Après une étude précise des intensités de diffraction sur poudre aux rayons X et aux neutrons, nous confirmons ici l'isomorphisme de BaSrFe<sub>4</sub>O<sub>8</sub> et BaCaFe<sub>4</sub>O<sub>8</sub>.