

## The Crystal Structure of $\text{CaCl}_2 \cdot \text{glycylglycylglycine} \cdot 3\text{H}_2\text{O}$ \*

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The crystal structure of  $\text{CaCl}_2(\text{glycylglycylglycine}) \cdot 3\text{H}_2\text{O}$  has been determined and refined by three-dimensional least-squares techniques based on 2327 intensities measured on a diffractometer. The crystals are triclinic, space group  $P\bar{1}$ , with  $a = 6.961$ ,  $b = 8.558$ ,  $c = 12.115$  Å,  $\alpha = 85.82^\circ$ ,  $\beta = 91.49^\circ$  and  $\gamma = 94.28^\circ$ . The final  $R$  value for 2327 reflections is 0.114; the standard deviations are about 0.01 Å for the positions of the C, N and O atoms. The tripeptide molecule is in the form of the zwitterion. The  $\text{Ca}^{2+}$  ion is bonded to seven oxygen atoms from four different peptide molecules and two water molecules which form an approximate pentagonal bipyramid. Each  $\text{Cl}^-$  ion accepts hydrogen bonds from two water molecules, from an amide NH group of one peptide molecule and from the terminal  $\text{NH}_3^+$  group of another peptide molecule. The peptide molecules are held together by means of this complex hydrogen-bond network which makes use of all the available hydrogen atoms for hydrogen bonding, and by means of the bonding of the  $\text{Ca}^{2+}$  ion to the oxygen atoms of different peptide molecules. There is no hydrogen bonding between the peptide molecules themselves.

### Introduction

The determination of the structure of  $\text{CaCl}_2(\text{glycylglycylglycine}) \cdot 3\text{H}_2\text{O}$  was undertaken as a part of an overall program for studying the influence of metal ions on the conformation of peptides. This study is being carried out primarily on compounds which have been crystallized from neutral solutions. The Ca complex was of particular interest for it afforded an opportunity to study interactions between a non-transition metal and a peptide.

### Experimental

Crystals of  $\text{CaCl}_2(\text{glycylglycylglycine}) \cdot 3\text{H}_2\text{O}$  were obtained by evaporation of an aqueous solution containing equimolar amounts of glycylglycylglycine (ggg) and  $\text{CaCl}_2$ . This compound was first prepared by Pfeiffer (1927). The crystals grown in this manner were almost invariably twinned; however, it was found that crystals with only a small percentage of twinning could be obtained by adding a large excess of  $\text{CaCl}_2$  to the solution before evaporation. Colorless rectangular crystalline plates belonging to the triclinic system were obtained in this manner. The plate face was chosen as the (001) plane. Cell dimensions determined at  $22^\circ\text{C}$  by least-squares analysis were calculated to be  $a = 6.961 \pm 0.002$ ,  $b = 8.558 \pm 0.002$ ,  $c = 12.115 \pm 0.003$  Å,  $\alpha = 85.82 \pm 0.03^\circ$ ,  $\beta = 91.49 \pm 0.02^\circ$  and  $\gamma = 94.28 \pm 0.04^\circ$  ( $\lambda(\text{Cu } K\alpha) = 1.5418$  Å). The F.W. for  $\text{CaCl}_2(\text{ggg}) \cdot 3\text{H}_2\text{O}$  is 354.22, yielding  $\rho_c = 1.64$  g.cm $^{-3}$ ; the observed density measured by flotation is  $\rho_o = 1.63$  g.cm $^{-3}$ . There are two formula units in the unit cell. The space group was assumed to be the centric  $P\bar{1}$  and, indeed, this was demonstrated by  $N(z)$  test (Howells, Phillips & Rogers, 1950) from all of the data (Willoughby, 1968). The Delaunay

reduced cell has dimensions  $a' = 10.622$ ,  $b' = 14.315$ ,  $c' = 12.115$  Å,  $\alpha' = 143.40^\circ$ ,  $\beta' = 92.39^\circ$  and  $\gamma' = 114.66^\circ$  and can be obtained by the transformation matrix

$$S = \begin{pmatrix} 1 & 1 & 0 \\ 0 & -1 & 1 \\ 0 & 0 & -1 \end{pmatrix}. \text{ The angle } \alpha' \text{ especially is awkward and}$$

it was therefore decided to use the former cell.

Four different crystals were used in obtaining the intensity data. The crystals were thin rectangular plates with largest dimensions ranging from 0.1 mm to 0.4 mm. The integrated intensities were taken on a General Electric XRD-5 diffractometer unit equipped with a single-crystal orienter, a scintillation counter and a pulse-height analyzer, using the  $\theta$ - $2\theta$  scan method and Ni-filtered Cu  $K\alpha$  radiation. A total of 2327 reflections were measured below a  $2\theta$ -value of  $145^\circ$ . This represents all of the reflections within a  $2\theta$ -limit of  $110^\circ$  and approximately one-third of the reflections between  $110^\circ$  and  $145^\circ$ . Of the 2327 reflections, 346 did not show a peak on the recorder while scanning through their diffraction position. The intensities recorded for these unobserved reflections was a fraction of the background intensity measured at the location of the reflection. Lorentz, polarization and absorption corrections ( $\mu = 73.8$  cm $^{-1}$ ) were applied to the data.

### Structure determination

The sharpened Patterson synthesis could be interpreted for three different sets of positions for the Ca and two Cl ions. For one set of positions the Patterson map was further interpreted yielding the positions of 6 oxygen atoms surrounding the Ca ion at distances ranging from 2.2 to 2.6 Å (Willoughby, 1968). Structure-factor calculations were made and the first Fourier synthesis using the signs of the structure factors determined by the Ca, two Cl and six oxygen atoms yielded the locations of all other atoms present in the structure.

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The first structure-factor calculation with all atoms given isotropic temperature factors resulted in an

$$R \left( = \frac{\sum ||KF_o| - |F_c||}{\sum |KF_o|} \right) \text{ of } 0.24. \text{ Structure-factor least-}$$

squares cycles with isotropic temperature factors for all atoms reduced the  $R$  value to 0.18. At this point the Ca, 2 Cl and 7 O atoms were given anisotropic temperature factors and the structure was further refined by block-diagonal least-squares computations to an  $R$  value of 0.13. Refining the structure further with all atoms given anisotropic temperature factors did not significantly lower the  $R$  value.

At this point the observed structure factor amplitudes were corrected for anomalous dispersion (Patterson, 1963). The positions of the hydrogen atoms were calculated. This calculation was possible for all hydrogen atoms either from the geometry of the molecule or from the predicted hydrogen-bonding scheme (See *Discussion of the structure*). A difference Fourier synthesis was then calculated showing peaks at 11 of the 17 positions calculated for the hydrogen atoms. The 11 hydrogen atoms were included in the subsequent structure-factor calculations but their parameters were not refined. The positional and anisotropic thermal parameters of the calcium, chlorine, carbon, oxygen and nitrogen atoms were further refined by block-diagonal least-squares methods until the parameter shifts for the coordinates were less than  $1/15 \sigma$ , and for the temperature factors less than  $1/5 \sigma$ , in which  $\sigma$  is the calculated standard deviation. A second difference map was then calculated based on a structure-factor calculation which did not include the hydrogen atom contributions. The 11 hydrogen atoms which had been found in the first difference map were relocated but the remaining 6 hydrogen atoms still could not be located. Peak heights and parameters of the 11 hydrogen atoms still could not be located. Peak heights and par-

ameters of the 11 hydrogen atoms are given in Table 4. The maximum spurious peaks in the difference map were  $+0.7$  and  $-1.2 \text{ e} \cdot \text{\AA}^{-3}$ . The map did not indicate any significant coordinate shifts for the non-hydrogen atoms. The quantity minimized in the least-squares calculations was  $\sum w(|KF_o| - |F_c|)^2$ . The final weighting scheme used was  $\sqrt{w} = |KF_o|/P$  if  $|KF_o| \leq P$  and  $\sqrt{w} = P/|KF_o|$  if  $|KF_o| > P$  ( $P = 15.0$  electrons). The final positional and thermal parameters and their estimated standard deviations, as calculated from the inverse of the least-squares matrix, for all atoms except hydrogens are given in Tables 1 and 2. The final  $R$  value for all data is 0.114. The principal axes of the thermal ellipsoids were determined and the magnitudes together with their direction cosines with respect to the cell edges are listed in Table 5. A list of calculated and observed structure factors is given in Table 3. The SFLS program used was written by Ahmed (1966). A

Table 1. *Final atomic positions*

Standard deviations are given in parentheses.

	<i>x</i>	<i>y</i>	<i>z</i>
Ca	0.4161 (3)	0.1418 (2)	0.8719 (2)
Cl(1)	0.2934 (6)	0.2057 (4)	0.4999 (3)
Cl(2)	0.1767 (4)	0.6669 (3)	0.6824 (2)
N(1)	0.2571 (17)	0.7706 (11)	0.4327 (8)
C <sup>α</sup> (1)	0.2246 (17)	0.6079 (12)	0.4045 (8)
C'(1)	0.3008 (14)	0.5888 (12)	0.2894 (8)
O(1)	0.3333 (11)	0.7001 (8)	0.2241 (6)
N(2)	0.3234 (12)	0.4398 (9)	0.2684 (6)
C <sup>α</sup> (2)	0.3950 (14)	0.4003 (11)	0.1667 (9)
C'(2)	0.2577 (13)	0.3450 (10)	0.0771 (8)
O(2)	0.3178 (10)	0.3192 (8)	-0.0119 (5)
N(3)	0.0675 (12)	0.3267 (8)	0.0986 (6)
C <sup>α</sup> (3)	-0.0785 (15)	0.2821 (12)	0.0214 (8)
C'(3)	-0.1744 (15)	0.1192 (11)	0.0458 (7)
O(3)	-0.3273 (10)	-0.0854 (8)	-0.0074 (6)
O(4)	-0.1130 (10)	0.0258 (8)	0.1196 (5)
O <sub>w</sub> (1)	0.1382 (11)	0.0315 (9)	0.2930 (7)
O <sub>w</sub> (2)	0.2315 (13)	0.2939 (9)	0.7392 (6)
O <sub>w</sub> (3)	0.5307 (13)	0.0367 (9)	0.2592 (7)

Table 2. *Final anisotropic thermal parameters\**

Standard deviations in parentheses.

	$B_{11}$	$B_{22}$	$B_{33}$	$B_{23}$	$B_{13}$	$B_{12}$
Ca	0.0143 (4)	0.0046 (2)	0.0030 (1)	0.0006 (3)	-0.0007 (4)	-0.0005 (5)
Cl(1)	0.0417 (12)	0.0141 (5)	0.0049 (2)	-0.0009 (5)	-0.0048 (8)	0.0011 (12)
Cl(2)	0.0183 (6)	0.0108 (4)	0.0046 (2)	-0.0021 (4)	0.0023 (5)	-0.0009 (8)
N(1)	0.0398 (35)	0.0086 (14)	0.0047 (7)	-0.0009 (16)	0.0026 (25)	0.0020 (35)
C <sup>α</sup> (1)	0.0210 (28)	0.0080 (15)	0.0044 (7)	0.0015 (17)	0.0017 (23)	-0.0046 (32)
C'(1)	0.0123 (22)	0.0092 (15)	0.0041 (7)	-0.0027 (16)	-0.0067 (20)	-0.0042 (29)
O(1)	0.0189 (18)	0.0068 (10)	0.0048 (5)	0.0040 (11)	0.0029 (15)	-0.0040 (21)
N(2)	0.0166 (21)	0.0080 (13)	0.0024 (5)	-0.0018 (13)	0.0002 (16)	-0.0037 (25)
C <sup>α</sup> (2)	0.0129 (23)	0.0066 (14)	0.0060 (8)	0.0018 (17)	-0.0033 (22)	0.0038 (28)
C'(2)	0.0117 (21)	0.0039 (12)	0.0042 (7)	-0.0003 (14)	-0.0033 (19)	0.0007 (24)
O(2)	0.0142 (16)	0.0101 (11)	0.0041 (5)	-0.0064 (12)	0.0060 (14)	-0.0016 (21)
N(3)	0.0215 (22)	0.0028 (10)	0.0029 (5)	0.0028 (11)	-0.0069 (17)	-0.0050 (23)
C <sup>α</sup> (3)	0.0141 (24)	0.0083 (15)	0.0048 (7)	0.0048 (17)	-0.0041 (21)	-0.0093 (29)
C'(3)	0.0187 (26)	0.0073 (14)	0.0030 (6)	0.0002 (15)	0.0045 (21)	-0.0035 (30)
O(3)	0.0127 (16)	0.0101 (11)	0.0069 (6)	0.0056 (13)	-0.0059 (16)	-0.0127 (21)
O(4)	0.0168 (17)	0.0064 (9)	0.0046 (5)	0.0035 (11)	-0.0038 (14)	-0.0021 (20)
O <sub>w</sub> (1)	0.0184 (19)	0.0140 (13)	0.0071 (6)	-0.0051 (15)	-0.0081 (18)	0.0154 (25)
O <sub>w</sub> (2)	0.0295 (24)	0.0108 (13)	0.0052 (6)	-0.0009 (13)	-0.0040 (19)	0.0103 (27)
O <sub>w</sub> (3)	0.0254 (22)	0.0089 (12)	0.0080 (7)	-0.0047 (14)	0.0052 (20)	-0.0023 (25)

\* Temperature factor =  $\exp [-(h^2 B_{11} + k^2 B_{22} + l^2 B_{33} + hk B_{12} + hl B_{13} + kl B_{23})]$ .

logical routine has been added to this program such that reflections which are clearly observational errors, as for instance 010, are excluded from the least-squares

refinement. This logical routine also excludes most of the reflections affected by extinction from the least-squares sums. The atomic scattering factors used for

Table 3. Observed and calculated structure factors

The listing shows for each reflection h, |10KF<sub>o</sub>| and 10F<sub>c</sub>. The reflections for which the intensity could not be distinguished from the background are indicated by a star.

Table with multiple columns for reflection indices (h, k, l) and intensity values (|10KFo|, 10Fc). The table lists various reflections such as 1 140 -83, 2 127 800, etc., with corresponding intensity values and calculated structure factors.



Table 5. Values of anisotropic temperature factors along the principal axes

Values of the temperature factors (in Å<sup>2</sup>) along the major, intermediate and minor axes of the thermal ellipsoids are given together with the direction cosines of these axes with respect to the axes of the crystallographic unit cell.

	$B_i$	$l_1$	$l_2$	$l_3$
Ca	2.86	0.970	-0.220	-0.227
	1.81	0.236	0.388	0.903
	1.23	0.052	0.895	-0.365
Cl(1)	8.27	0.986	-0.129	-0.188
	4.07	0.053	0.992	0.050
	2.70	0.159	0.000	0.981
Cl(2)	3.86	0.831	-0.504	0.281
	2.95	0.499	0.821	-0.052
	2.51	-0.244	0.268	0.958
N(1)	7.70	0.997	-0.059	0.050
	2.72	-0.075	0.026	0.997
	2.50	-0.014	0.998	0.050
C <sup>α</sup> (1)	4.40	0.945	-0.397	-0.030
	2.93	0.164	0.506	0.869
	1.78	0.284	0.766	-0.494
C'(1)	3.71	-0.757	0.382	0.607
	2.89	-0.046	0.839	-0.482
	0.93	0.652	0.388	0.631
O(1)	3.94	0.949	-0.384	-0.033
	3.50	0.163	0.518	0.862
	1.18	0.268	0.764	-0.506
N(2)	3.58	0.900	-0.496	0.012
	2.08	0.427	0.811	-0.271
	1.32	0.082	0.310	0.962
C <sup>α</sup> (2)	3.92	-0.377	0.262	0.920
	2.52	0.788	0.529	0.198
	1.51	-0.486	0.807	-0.339
C'(2)	2.99	-0.664	0.111	0.764
	1.76	0.748	0.007	0.644
	1.12	-0.006	0.994	-0.016
O(2)	4.30	-0.529	0.609	-0.572
	2.44	0.741	0.614	0.015
	1.13	-0.414	0.502	0.820
N(3)	5.05	0.896	-0.294	-0.420
	1.36	0.444	0.410	0.796
	0.49	0.007	0.863	-0.436
C <sup>α</sup> (3)	4.61	-0.681	0.606	0.531
	2.29	0.320	-0.381	0.841
	1.33	0.649	0.698	0.101
C'(3)	4.00	0.931	-0.307	0.235
	2.20	0.083	0.867	0.535
	1.36	-0.356	-0.392	0.812
O(3)	6.31	-0.513	0.620	0.682
	2.51	-0.460	0.465	-0.731
	1.09	0.724	0.632	-0.017
O(4)	4.22	0.716	-0.437	-0.627
	2.44	0.697	0.387	0.578
	1.34	-0.039	0.812	-0.523
Ow(1)	6.22	0.575	0.518	-0.567
	3.28	0.067	0.684	0.765
	1.94	-0.815	0.514	-0.305

Table 5 (cont.)

	$B_i$	$l_1$	$l_2$	$l_3$
Ow(2)	6.06	0.928	0.226	-0.228
	3.11	-0.037	0.676	0.783
	2.59	-0.370	0.701	-0.578
Ow(3)	5.78	0.724	-0.261	0.622
	4.00	-0.686	-0.072	0.724
	2.30	0.067	0.963	0.298

of the first residue in ggg are denoted N(1)C<sup>α</sup>(1)C'(1)-O(1). The oxygen atoms of the three water molecules are labeled Ow(1), Ow(2) and Ow(3).

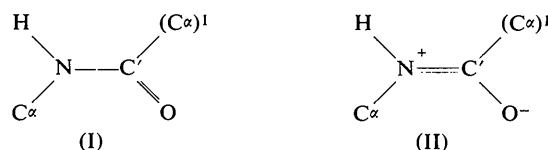
#### Geometry and conformation of the peptide molecule

Bond lengths and angles in the peptide molecule are shown in Figs. 2 and 3. Average values for free peptides have been tabulated by Marsh & Donohue (1967) (Table 6). The C<sup>α</sup>-C' distances of 1.53, 1.51 and 1.51 Å are in close agreement with the average value of 1.51 Å. Except for the terminal C<sup>α</sup>-NH<sub>3</sub><sup>+</sup> distance, the N-C<sup>α</sup> distances of 1.41 and 1.41 Å are shorter than the average value of 1.45 Å. The C'-N bond lengths of 1.34 and 1.35 Å are consistently longer than the average value of 1.32 Å and C'-O bond lengths of 1.21 and 1.21 Å are shorter than the average value of 1.24 Å. These differences are thought to be significant considering their consistency and the estimated standard deviations of the bond lengths.

Table 6. Reference bond lengths and angles in peptides

Peptides (Marsh & Donohue, 1967)		Metal-complexes of peptides (Freeman, 1967)
Bond	Length	Length
N-C <sup>α</sup> (terminal)	1.49 Å	1.49 Å
C <sup>α</sup> -C'	1.51	1.53
C'-O	1.24	1.26
C'-N	1.325	1.30
N-C <sup>α</sup>	1.455	1.46
Angle		
	$\theta$	$\theta$
NC <sup>α</sup> C'	111°	111°
C <sup>α</sup> C'N	116	115
C <sup>α</sup> C'O	120.5	119
OC'N	123.5	126
C'NC <sup>α</sup>	122	123

The shortness of the C'-N bond in peptide linkages, 1.32 Å, can be attributed to partial double bond character as can be shown from the two resonance forms



To explain the longer than normal C'-N distances and the shorter than normal C'-O distances in the Ca complex, it is assumed that resonance form (I) contributes

more to the actual structure than is normally the case when the peptide is not complexed. This is the exact opposite of the trend in the Cu-peptide complexes, where the average C'-N distance of 1.30 Å and the average C'-O distance of 1.26 Å indicate a greater than normal contribution of resonance form (II) (Freeman, 1966) (Table 6). It should be pointed out that these averages are weighted to structures where the peptide nitrogen atom has been deprotonated and is chelated to the Cu atom. Other transition metal complexes of peptides also show this trend (Freeman, 1967). In the Ca-peptide complex both peptide oxygens are bonded to Ca ions, Fig. 1. It may be that the standard deviations in the present structure are underestimated but it will

be interesting to see if the deviations in the C'-O and C'-N bond lengths found in the Ca complex are characteristic of changes that occur in Ca-peptide complexes and in general non-transition metal complexes.

There seems to be no adequate explanation for the shorter than normal N-C $\alpha$  bond lengths of the second and third residues. Although the N-C $\alpha$  distance of 1.46 Å involving the terminal NH $_3^+$  group is appreciably longer than the other N-C $\alpha$  distances, it is also shorter than the average value of 1.49 Å found in other structures.

Bond angles in the peptide molecule are in fairly close agreement with the average values tabulated by Marsh & Donohue. The only significant differences are

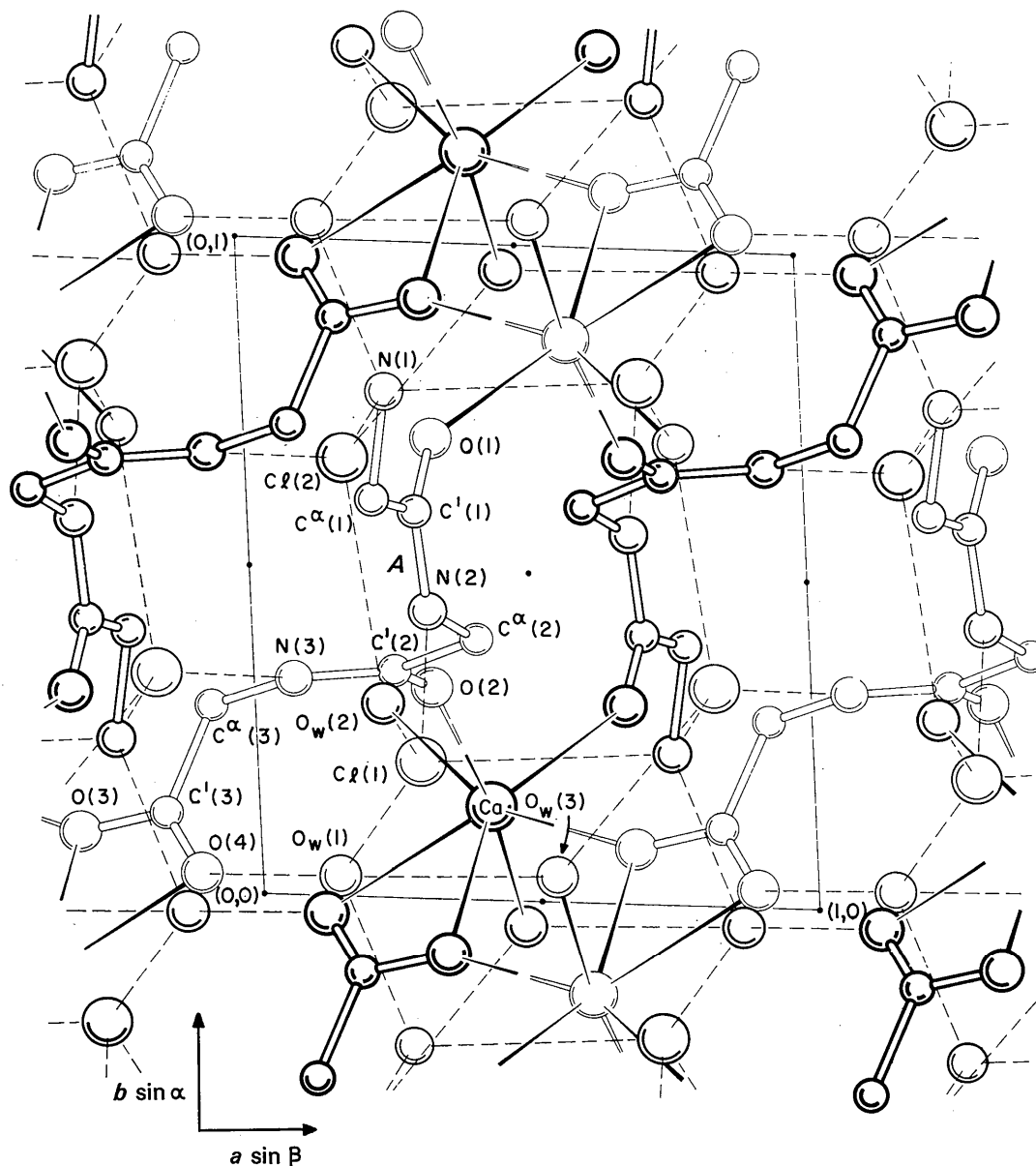


Fig. 1. View of the structure down the  $c$  axis.

in the N-C $\alpha$ -C' angles of the second and third residues. These are 120° and 115°, respectively, and are significantly larger than the average value of 111°. The N-C $\alpha$ -C' angle involving the terminal NH $_3^+$  group has the normal value of 111°.

The conformational angles  $\phi$ ,  $\psi$  and  $\omega$  (Edsall *et al.*, 1966) for each residue are given in Table 7. The values of  $\phi$  and  $\psi$  for each residue lie in the allowed regions of the conformation map calculated for glycyI residues (Ramakrishnan & Ramachandran, 1965) with the angle

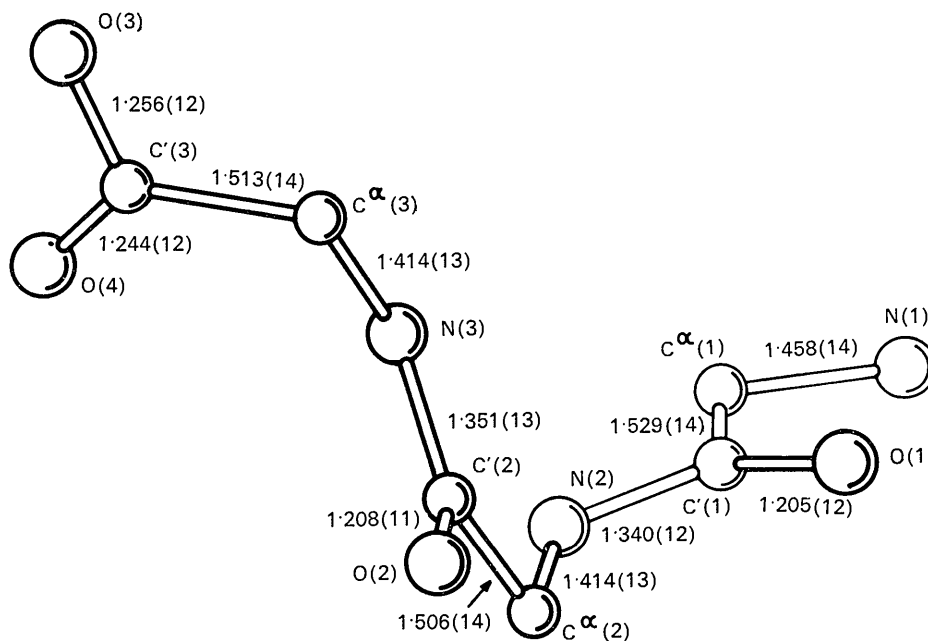


Fig. 2. Bond distances in the peptide molecule. Standard deviations in parentheses.

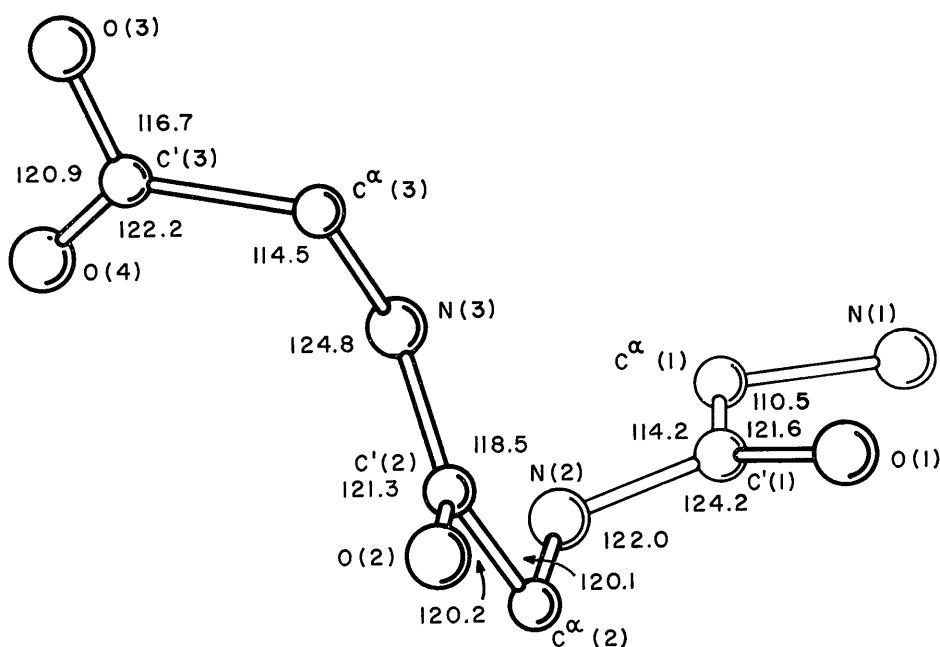


Fig. 3. Bond angles in the peptide molecule. Standard deviations between 0.8 and 0.9°.

$\text{N}-\text{C}^\alpha-\text{C}'$  equal to  $115^\circ$ . It should be pointed out, however, that the second residue is the only non-terminal residue in glycyglycylglycine and that the value of  $\varphi$  and  $\psi$  for this residue lie in the allowed region only when the 'outer limit' contact distances are used.

Table 7. Conformational angles

Residue	$\varphi$	$\psi$	$\omega$	$\text{N}-\text{C}^\alpha-\text{C}'$
1	—	$342.2^\circ$	$2.1^\circ$	$110.5^\circ$
2	$81.7^\circ$	176.1	357.8	120.1
3	290.5	351.5	—	114.5

The large  $\text{N}-\text{C}^\alpha-\text{C}'$  angles for the second and third residues give the peptide groups increased rotational freedom. The second residue has a somewhat unusual conformation in that the nitrogen atom [N(2)] is lying *trans* to the carbonyl oxygen atom [O(2)] and is therefore *cis* to the nitrogen atom of the third residue ( $\psi_2$  is  $176^\circ$ , Table 7). This is opposite to the strong tendency in small peptides for the amino or peptide nitrogens to be as close as possible to the carbonyl oxygen atom of the same residue (Leung & Marsh, 1958). Although the present conformation is unusual, it is thought to have occurred in order to utilize more fully the hydrogen-bonding capabilities of both peptide nitrogen atoms while leaving the carbonyl oxygen atom [O(2)] more available for bonding to the Ca ion; these facts may be correlated with the large N(2) C $^\alpha$ (2) C'(2) angle. The *cis* arrangement for the peptide nitrogen atoms of adjacent residues is also found in the transition metal complexes of tri- and higher peptides prepared from alkaline solutions (Freeman, 1967). Here the *cis* conformation is more of a necessity in that the peptide nitrogen atoms of adjacent residues have been deprotonated and are both coordinated to the same metal atom. In these structures, however, there seem to be no significant deviations of the  $\text{N}-\text{C}^\alpha-\text{C}'$  angles from their normal value of  $111^\circ$ .

In addition to the constancy of the bond lengths and angles of the peptide, the most important characteristic which is common to the peptides whose structures have been determined is the approximate planarity of the group of atoms  $\text{C}_i^\alpha \text{C}_i' \text{O}_i \text{N}_{i+1} \text{C}_{i+1}^\alpha$ . If this group of

atoms is not planar it is most often caused by a displacement of  $\text{C}_{i+1}^\alpha$ , which in turn is qualitatively reflected in a non-zero value of  $\omega_i$ . It was therefore decided to calculate least-squares planes (Schomaker, Waser, Marsh & Bergman, 1959) through the  $\text{C}_i^\alpha \text{C}_i' \text{O}_i \text{N}_{i+1}$  and  $\text{C}_i^\alpha \text{C}_i' \text{O}_i \text{N}_{i+1} \text{C}_{i+1}^\alpha$  groups and through the acid group (Table 8). The largest deviation is observed for  $\text{C}^\alpha(3)$  which is  $0.054 \text{ \AA}$  out of plane III.

#### Coordination of the Ca ion

The Ca ion is bonded to oxygen atoms from four different peptide molecules and is therefore very important in determining the packing of the peptides. In all it is bonded to seven oxygen atoms (Fig. 1 and 4) forming an approximate pentagonal bipyramid. Two of the oxygen atoms are centrosymmetrically related and are therefore shared by a second Ca ion. Seven-coordinated Ca ions have been reported elsewhere in the literature, for example, in dicalcium phosphate dihydrate (MacLennan & Beevers, 1955), where both seven and eight coordinated Ca ions are present, and

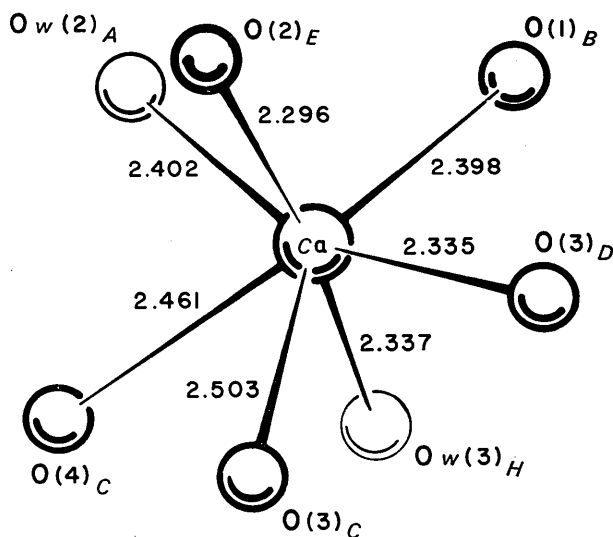
Fig. 4. Bond distances in the Ca-surrounding. Standard deviations are  $0.008 \text{ \AA}$ .

Table 8. Least-squares planes

Equations are expressed in the form  $Ax + By + Cz = D$ , where  $D$  is expressed in  $\text{Å}$ , and  $x$ ,  $y$  and  $z$  are fractional coordinates.

Plane	Atoms				A	B	C	D
I	$\text{C}^\alpha(1)$	$\text{C}'(1)$	$\text{O}(1)$	$\text{N}(2)$	6.4475	0.4557	4.1208	3.3941
II	$\text{C}^\alpha(1)$	$\text{C}'(1)$	$\text{O}(1)$	$\text{N}(2)$	6.4347	0.4924	4.1651	3.4265
III	$\text{C}^\alpha(2)$	$\text{C}'(2)$	$\text{O}(2)$	$\text{N}(3)$	-1.1504	8.0329	-3.1517	2.2346
IV	$\text{C}^\alpha(2)$	$\text{C}'(2)$	$\text{O}(2)$	$\text{N}(3)$	-1.0611	8.0529	-3.1153	2.2718
V	$\text{C}^\alpha(3)$	$\text{C}'(3)$	$\text{O}(3)$	$\text{O}(4)$	-4.1449	3.9429	8.8406	1.6199

Atoms	$\Delta(\text{I})$	$\Delta(\text{II})$	Atoms	$\Delta(\text{III})$	$\Delta(\text{IV})$	Atoms	$\Delta(\text{V})$
$\text{C}^\alpha(1)$	-0.002 $\text{Å}$	0.003 $\text{Å}$	$\text{C}^\alpha(2)$	-0.001 $\text{Å}$	-0.013 $\text{Å}$	$\text{C}^\alpha(3)$	-0.006 $\text{Å}$
$\text{C}'(1)$	0.006	0.004	$\text{C}'(2)$	0.003	0.007	$\text{C}'(3)$	0.022
$\text{O}(1)$	-0.002	-0.004	$\text{O}(2)$	-0.001	0.002	$\text{O}(3)$	-0.008
$\text{N}(2)$	-0.002	-0.011	$\text{N}(3)$	-0.001	0.020	$\text{O}(4)$	-0.008
$\text{C}^\alpha(2)$	0.022	0.007	$\text{C}^\alpha(3)$	-0.054	-0.016		



in calcium thymidylate (Trueblood, Horn & Luzzatti, 1961). Ca ions exhibiting coordination numbers of anywhere from six to nine have been reported in the structures of phosphates and silicates.

The five oxygen atoms which form the pentagonal arrangement consist of a carbonyl oxygen atom  $O(1)_B$  of one peptide molecule at a distance of 2.40 Å, an oxygen atom of a water molecule  $Ow(2)_A$  at 2.40 Å, both oxygen atoms  $O(3)_C$  and  $O(4)_C$  of a carboxylate group of a second peptide molecule at distances of 2.50 and 2.46 Å, and one oxygen atom  $O(3)_D$  of a carboxylate group of a third peptide molecule at a distance of 2.34 Å (subscript notation is explained in Table 9). Bonded on one side of this plane is a carbonyl oxygen atom  $O(2)_E$  of a fourth peptide molecule at a distance of 2.30 Å and on the other side of the plane an oxygen atom  $Ow(3)_H$  of a water molecule at a distance 2.43 Å. These bond lengths are in the normal range of 2.2 to 2.6 Å for Ca–O bonds. Bond angles in the Ca-surrounding are given by Willoughby (1968). The two Ca ions which share in the bonding of two centrosymmetrically related oxygen atoms are 4.00 Å apart. It is interesting to note that this is very close to the Ca–Ca distance of 3.95 Å found in the  $\alpha$ -form of Ca.

Table 9. Symmetry operations used in Table 10, Fig. 4 and in the text

Subscript	Coordinates		
<i>A</i>	<i>x</i>	<i>y</i>	<i>z</i>
<i>B</i>	1– <i>x</i>	1– <i>y</i>	1– <i>z</i>
<i>C</i>	– <i>x</i>	– <i>y</i>	1– <i>z</i>
<i>D</i>	1+ <i>x</i>	<i>y</i>	1+ <i>z</i>
<i>E</i>	<i>x</i>	<i>y</i>	1+ <i>z</i>
<i>F</i>	– <i>x</i>	1– <i>y</i>	1– <i>z</i>
<i>G</i>	<i>x</i>	1+ <i>y</i>	<i>z</i>
<i>H</i>	1– <i>x</i>	– <i>y</i>	1– <i>z</i>
<i>K</i>	<i>x</i>	–1+ <i>y</i>	<i>z</i>

There is no bonding of the Ca ions to the Cl ions. In this respect the structure is similar to that of the cyclic amine complex  $CaBr_2 \cdot 10H_2O \cdot 2(CH_2)_6N_4$  (Mazzarella, Kovacs, DeSantis & Liquori, 1967) where  $Ca(H_2O)_6^{2+}$  octahedra are formed but no Ca–Br bonds.

With the Ca ion being surrounded only by oxygen atoms, the Cl ions are used to fill in the many hydrogen bonding sites found at the peptide and amino nitrogen atoms and at the water molecules.

#### Details of the hydrogen bonding

The terminal  $NH_3^+$  group forms three hydrogen bonds. Two bonds are formed with  $Cl^-$  ions and one to an oxygen atom of a water molecule. The N...Cl distances are 3.14 Å (to  $Cl(2)_A$ ) and 3.21 Å [to  $Cl(1)_B$ ]. These distances fall within the range of distances observed for  $NH_3^+ \dots Cl$  hydrogen bonds observed in hydrochloride structures of amino acids and peptides. The third hydrogen bond formed by the  $NH_3^+$  group is to  $Ow(1)_G$ , the distance being 2.86 Å, which is a normal value for a N–H...O hydrogen bond. The terminal N atom ( $NH_3^+$ ) is approximately tetrahedrally surrounded by  $C^\alpha(1)$ , two chloride ions, and the oxygen atom of a water molecule. It is therefore expected that the H atoms are directed towards the Cl ions and the oxygen atom; however, only one of these positions corresponded to a peak in the difference electron density map. These H-bond distances and angles are given in Table 10.

The hydrogen atoms attached to the peptide nitrogen atoms N(2) and N(3), form hydrogen bonds with respectively  $Cl(1)_A$  and  $Cl(2)_F$ . The surrounding of both peptide nitrogen atoms is plane trigonal (Table 10).

Both  $Cl^-$  ions accept four hydrogen bonds, including one bond each from a terminal amino group and a peptide nitrogen atom. In addition they both accept 2 hydrogen bonds from water molecules, at distances ranging between 3.10 and 3.26 Å (Table 10). These fall in the range of normal (Parthasarathy, 1960) or average (Clark, 1963) values for O–H...Cl bonds. The arrangements of the hydrogen bonds around the  $Cl^-$  ions are approximately tetrahedral (Fig. 1).

The water molecule which is not bonded to the Ca ion [ $Ow(1)_A$ ] forms four hydrogen bonds, donating two bonds to  $O(4)_A$  and  $Cl(1)_A$  while accepting bonds from  $N(1)_K$  and  $Ow(3)_A$ . The water molecules which are bonded to the Ca ion,  $Ow(2)$  and  $Ow(3)$ , are each the donors in the formation of two hydrogen bonds. The hydrogen bonds around  $Ow(1)$  are approximately tetrahedral with

Table 10. Hydrogen bond lengths and angles

Standard deviations are given in parentheses.

Bond	Length (Å)	Angle	Angle (°)
$N(1)_A-H \dots Cl(1)_B$	3.209 (13)	$Cl(2)_A-N(1)_A-Cl(1)_B$	87.1
$N(1)_A-H \dots Cl(2)_A$	3.142 (10)	$Cl(2)_A-N(1)_A-Ow(1)_G$	131.5
$N(1)_A-H \dots Ow(1)_G$	2.861 (13)	$C^\alpha(1)_A-N(1)_A-Cl(2)_A$	90.2
$Ow(1)_A-H \dots Cl(1)_A$	3.136 (9)	$C^\alpha(1)_A-N(1)_A-Cl(1)_B$	102.3
$Ow(1)_A-H \dots O(4)_A$	2.699 (10)	$C^\alpha(1)_A-N(1)_A-Ow(1)_G$	123.4
$Ow(2)_A-H \dots Cl(1)_A$	3.097 (8)	$Cl(1)_B-N(1)_A-Ow(1)_G$	114.2
$Ow(2)_A-H \dots Cl(2)_A$	3.264 (8)	$C'(1)_A-N(2)_A-Cl(1)_A$	110.7
$Ow(3)_A-H \dots Cl(2)_B$	3.240 (9)	$C^\alpha(2)_A-N(2)_A-Cl(1)_A$	125.7
$Ow(3)_A-H \dots Ow(1)_A$	2.770 (12)	$C'(2)_A-N(3)_A-Cl(2)_F$	133.9
$N(2)_A-H \dots Cl(1)_A$	3.327 (8)	$C^\alpha(3)_A-N(3)_A-Cl(2)_F$	101.1
$N(3)_A-H \dots Cl(2)_F$	3.194 (8)	$Cl(1)_A-Ow(1)_A-O(4)_A$	146.9
		$Cl(1)_A-Ow(2)_A-Cl(2)_A$	97.7
		$Cl(2)_B-Ow(3)_A-Ow(1)_A$	122.0

angles ranging between  $76^\circ$  ( $\text{Ow}(3)_A\text{--Ow}(1)_A\text{--N}(1)_K$ ] and  $147^\circ$  [ $\text{Cl}(1)_A\text{--Ow}(1)_A\text{--O}(4)_A$ ], while the arrangements around  $\text{Ow}(2)$  and  $\text{Ow}(3)$  are close to trigonal with the sum of the three angles for  $\text{Ow}(2)$  and  $\text{Ow}(3)$  being  $345$  and  $355^\circ$  respectively.

This hydrogen bond network makes use of all the hydrogen atoms available for this type of bonding. There is no intramolecular or intermolecular hydrogen bonding between peptide molecules. However, by means of a single intermediary, either a water molecule, a Cl ion or a Ca ion, one peptide is bonded to ten other peptide molecules.

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## Etude Cristallographique du Manganite Spinelle Cubique $\text{NiMn}_2\text{O}_4$ par Diffraction de Neutrons

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It is shown that the inversion parameter,  $\nu$ , in the cubic spinel ( $\text{Mn}_\nu\text{Ni}_{1-\nu}$ ) [ $\text{Mn}_{2-\nu}\text{Ni}_\nu$ ] $\text{O}_4$  changes from 0.74 when the sample is quenched from a high temperature to 0.93 when slowly cooled. The cell parameter is a linear function of  $\nu$  and is a minimum when  $\nu$  is a maximum; the oxygen positional parameter is independent of thermal treatment. The short range order between nickel and manganese atoms in the  $B$  sites was examined and the correlation coefficients were determined. The variation of internal energy as a function of the degree of inversion was also calculated and discussed.

### Introduction

Le manganite de nickel,  $\text{NiMn}_2\text{O}_4$ , est un spinelle cubique (Sinha, Sanjana & Biswas, 1957) (groupe d'espace  $Fd\bar{3}m$ ,  $O_h^7$ ). Villers & Buhl (1965) ont décrit en détail la méthode de fabrication de ce corps et ont montré que

certaines propriétés cristallines ou magnétiques variaient avec la température de trempe. Nous étudions ces échantillons par des mesures de diffraction de neutrons et déterminons la valeur des paramètres caractérisant la structure cristalline.

### Echantillons étudiés; contrôle de pureté

Les échantillons ont été préparés suivant la méthode décrite dans Villers & Buhl (1965). Le corps, formé à

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