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Structures of L-Prolylsarcosine Monohydrate and *tert*-Butoxycarbonyl-L-prolylsarcosine Benzyl Ester

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Abstract

The crystal structures of the title compounds have been determined by the X-ray method. The crystal data are: L-prolylsarcosine monohydrate, $P2_12_12_1$, a = 11·003 (4), b = 11·916 (3), c = 7·795 (2) Å, Z = 4, R = 0·097; *tert*-butoxycarbonyl-L-prolylsarcosine benzyl ester, $P2_12_12_1$, a = 11·271 (2), b = 18·751 (1), c = 9·372 (1) Å, Z = 4, R = 0·070. The conformations of the main chains of the two peptides agree well with each other. The peptide bonds between the prolyl and sarcosyl residues have *cis* configurations, and the bond angles around the N(Sar) atom are significantly affected by the configuration of the peptide bond. In the *cis* form, the angle C′—N—C^{α} is larger and C′—N—C^{Me} is smaller, both by about 6°, than those in the *trans* form. The conformational-energy calculation indicates that the stability of the *cis* peptide bond of the sarcosyl residue is almost equal to that of the *trans* form, and that the configuration may be determined by intramolecular interactions with other groups in the molecule and intermolecular forces.

Introduction

Sarcosine or *N*-methylglycine, which rarely occurs in proteins, is one of the major components of antibiotics, such as actinomycin or etamycin. The crystal structures of several cyclic peptides containing sarcosine have been reported (Groth, 1969, 1970, 1973*a*,*b*, 1974, 1975; Jain & Sobell, 1972; Declercq, Germain, Van Meerssche, Debaerdemaeker, Dale & Titlestad, 1975). In many of these, the *cis* form of the peptide bond was observed at the main-chain reversal points to form a ring. Because sarcosine has a substituent at the N atom, it may easily have a *cis* configuration in the cyclic peptide. However, very few structure analyses of such linear peptides have been published; one such structure is *tert*-butoxycarbonyl(Boc)-Sar-Gly-OBz (Itoh, Yamane, Ashida, Sugihara, Imanishi & Higashimura, 1976). Thus investigation of the conformation of the sarcosyl residue in linear peptides is particularly important in the examination of the conformational role of the sarcosyl residue in peptides. Linear peptides containing sarcosine, L-Pro-Sar, Boc-L-Pro-Sar, Boc-L-Pro-Sar-OBz and *tert*-amyloxycarbonyl(Aoc)-L-Pro-Sar-OBz, were prepared and crystallographic studies were undertaken. The structure of Boc-L-Pro-Sar has already been reported (Itoh, Yamane & Ashida, 1978). The crystals of Boc-L-Pro-Sar-OBz and Aoc-L-Pro-Sar-OBz are isomorphous with each other.

In this paper the crystal structures of L-Pro-Sar and Boc-L-Pro-Sar-OBz are dealt with and also a brief description of the conformational stability of L-Pro-Sar, Boc-L-Pro-Sar-OBz and Boc-L-Pro-Sar is presented.

Experimental

L-Pro-Sar was recrystallized by slow evaporation of an ethanol–water solution, and Boc-L-Pro-Sar-OBz was recrystallized from an ethanol–ether solution. Crystal data are given in Table 1, together with those of Aoc-L-Pro-Sar-OBz. Intensity data of both peptides were collected on a Hilger & Watts automatic four-circle diffractometer with Ni-filtered Cu $K\alpha$ radiation, the ω–2θ step-scan method being used. For L-Pro-Sar, 631

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Table 1. *Crystal data*

	L-Pro-Sar	Boc-L-Pro-Sar-OBz	Aoc-L-Pro-Sar-OBz
Formula	$C_8H_{14}N_2O_3.H_2O$	$C_{20}H_{28}N_2O_5$	$C_{21}H_{30}N_2O_5$
M_r	204·2	376·5	390·5
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions			
a	11·003 (4) Å	11·271 (2) Å	11·093 (2) Å
b	11·916 (3)	18·751 (1)	18·959 (4)
c	7·795 (2)	9·372 (1)	9·915 (2)
U	1022·0 Å^3	1980·7 Å^3	2084·1 Å^3
Z	4	4	4
D_m	1·329 Mg m^{-3}	1·261 Mg m^{-3}	1·234 Mg m^{-3}
D_x	1·328	1·262	1·245
Crystal size	0·30 × 0·60 × 0·02 mm	0·30 × 0·25 × 0·05 mm	0·20 × 0·20 × 0·30 mm
μ (Cu $K\alpha$)	0·857 mm^{-1}	0·707 mm^{-1}	0·688 mm^{-1}

reflections with $2\theta < 100°$ were collected, of which 583 were non-zero; for Boc-L-Pro-Sar-OBz 1551 reflections with $2\theta < 114°$ were collected, of which 1445 were non-zero. The intensity data were corrected for Lorentz and polarization effects, but no absorption correction was made.

Structure determination

Both structures were solved by the direct method with *MULTAN* (Germain, Main & Woolfson, 1971). The structures were refined by the block-diagonal least-squares method with *HBLS* V (Ashida, 1973), the H atoms being included in the refinement. Anisotropic and isotropic temperature factors were assigned to the non-H and H atoms, respectively. The function minimized was $\sum w(\Delta F)^2$, with $w = a$ for $|F_o| = 0$, and $w = [\sigma_{cs}^2(F) + b|F_o| + c|F_o|^2]^{-1}$ for $|F_o| > 0$, where $\sigma_{cs}(F)$ is the standard deviation based on counting statistics. In the final refinement, R was 0·097 with $a = 0·1373$, $b = -0·0166$, $c = 0·0006$ for L-Pro-Sar; R was 0·070 with $a = 0·1413$, $b = -0·0721$, $c = 0·0034$ for Boc-L-Pro-Sar-OBz. The atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1974). All calculations were made on the FACOM 230-75 computer of Nagoya University. The final parameters are listed in Tables 2 and 3.*

Table 2. L-Pro-Sar: *positional parameters* ($\times 10^4$, $\times 10^3$ *for* H) *with their standard deviations in parentheses*

	x	y	z
C(1)	377 (5)	7396 (4)	3672 (6)
C(2)	271 (5)	6319 (4)	4706 (7)
C(3)	210 (8)	5427 (5)	3407 (9)
C(4)	900 (6)	5771 (5)	1903 (8)
C(5)	1195 (5)	8285 (4)	4482 (7)
C(6)	1483 (5)	9786 (5)	6562 (8)
C(7)	−482 (5)	8757 (5)	6460 (6)
C(8)	−501 (5)	8188 (5)	8267 (6)
N(1)	1052 (4)	7023 (3)	2040 (5)
N(2)	723 (4)	8914 (3)	5762 (5)
O(1)	2241 (3)	8434 (3)	3967 (4)
O(2)	444 (3)	7831 (3)	8864 (4)
O(3)	−1521 (3)	8160 (3)	8960 (4)
O(W)	2674 (4)	6842 (5)	7732 (5)

	Bonded to	x	y	z
H(1)	C(1)	−41 (5)	777 (4)	334 (6)
H(2)	C(2)	−46 (5)	640 (4)	539 (6)
H(3)	C(2)	112 (4)	603 (4)	535 (7)
H(4)	C(3)	−60 (6)	545 (5)	291 (8)
H(5)	C(3)	47 (4)	461 (4)	381 (6)
H(6)	C(4)	44 (4)	573 (4)	89 (6)
H(7)	C(4)	177 (4)	535 (4)	168 (7)
H(8)	C(6)	180 (5)	1038 (4)	571 (8)
H(9)	C(6)	219 (5)	939 (4)	716 (7)
H(10)	C(6)	101 (6)	1012 (5)	736 (9)
H(11)	C(7)	−99 (4)	960 (3)	661 (5)
H(12)	C(7)	−106 (4)	836 (4)	566 (6)
H(13)	N(1)	184 (5)	700 (4)	210 (7)
H(14)	N(1)	84 (5)	737 (4)	85 (6)
H(15)	O(W)	204 (5)	712 (4)	781 (7)
H(16)	O(W)	299 (5)	686 (4)	893 (7)

Description of the structure

Molecular structure

The bond distances and angles are shown in Figs. 1 and 2. The mean e.s.d.'s of the distances and angles are 0·008 Å and 0·5° in L-Pro-Sar, and 0·006 Å and 0·4° in Boc-L-Pro-Sar-OBz, respectively. The torsion angles, defined by the IUPAC–IUB Commission on Biochemical Nomenclature (1970), are shown in Fig. 3. The equations of the best planes of several planar groups are listed in Tables 4 and 5.

The peptide bonds between the prolyl and sarcosyl residues of these peptides have the *cis* configuration, as

* Lists of structure factors and thermal parameters have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 34800 (15 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 3. Boc-L-Pro-Sar-OBz: *positional parameters* ($\times 10^4$, $\times 10^3$ *for* H) *with their standard deviations in parentheses*

	x	y	z
C(1)	2796 (3)	4505 (2)	10137 (6)
C(2)	762 (4)	4590 (2)	9190 (6)
C(3)	1089 (4)	4208 (2)	11724 (5)
C(4)	1571 (3)	4193 (1)	10225 (4)
C(5)	833 (3)	3005 (1)	9630 (4)
C(6)	2277 (3)	2298 (1)	8233 (4)
C(7)	2290 (3)	1492 (1)	7967 (4)
C(8)	974 (3)	1303 (1)	7753 (4)
C(9)	328 (3)	1813 (1)	8742 (4)
C(10)	2248 (3)	2702 (1)	6810 (4)
C(11)	3244 (3)	3140 (2)	4703 (4)
C(12)	4420 (3)	2538 (1)	6557 (4)
C(13)	5139 (3)	3149 (1)	7132 (4)
C(14)	7113 (3)	3470 (2)	7835 (4)
C(15)	7696 (3)	3899 (1)	6680 (4)
C(16)	8896 (3)	3803 (2)	6394 (4)
C(17)	9468 (3)	4211 (2)	5387 (5)
C(18)	8851 (3)	4710 (1)	4625 (4)
C(19)	7646 (3)	4814 (1)	4870 (5)
C(20)	7080 (3)	4411 (1)	5906 (4)
N(1)	1170 (2)	2391 (1)	9003 (3)
N(2)	3258 (2)	2761 (1)	6063 (3)
O(1)	1733 (2)	3466 (1)	9715 (3)
O(2)	−174 (2)	3103 (1)	10078 (2)
O(3)	1310 (2)	2935 (1)	6357 (2)
O(4)	4764 (2)	3726 (1)	7448 (3)
O(5)	6282 (1)	2953 (1)	7236 (2)

	Bonded to	x	y	z
H(1)	C(1)	279 (2)	503 (1)	1048 (4)
H(2)	C(1)	327 (3)	437 (1)	935 (4)
H(3)	C(1)	337 (3)	428 (1)	1081 (4)
H(4)	C(2)	57 (3)	504 (1)	959 (5)
H(5)	C(2)	−3 (3)	439 (1)	929 (4)
H(6)	C(2)	130 (3)	449 (2)	839 (5)
H(7)	C(3)	111 (3)	473 (2)	1210 (5)
H(8)	C(3)	179 (3)	393 (2)	1216 (6)
H(9)	C(3)	26 (3)	411 (2)	1165 (4)
H(10)	C(6)	297 (2)	244 (1)	880 (3)
H(11)	C(7)	261 (2)	124 (1)	882 (3)
H(12)	C(7)	278 (2)	131 (1)	727 (3)
H(13)	C(8)	79 (2)	72 (1)	780 (4)
H(14)	C(8)	79 (2)	140 (1)	670 (3)
H(15)	C(9)	−1 (3)	154 (2)	967 (4)
H(16)	C(9)	−43 (2)	204 (1)	836 (3)
H(17)	C(11)	390 (3)	332 (2)	425 (5)
H(18)	C(11)	290 (3)	369 (2)	489 (6)
H(19)	C(11)	258 (3)	300 (2)	412 (5)
H(20)	C(12)	433 (2)	219 (1)	728 (3)
H(21)	C(12)	480 (2)	230 (1)	575 (3)
H(22)	C(14)	662 (2)	379 (1)	840 (3)
H(23)	C(14)	773 (3)	322 (1)	831 (4)
H(24)	C(16)	935 (2)	346 (1)	694 (3)
H(25)	C(17)	1030 (2)	413 (1)	517 (3)
H(26)	C(18)	924 (2)	500 (1)	392 (4)
H(27)	C(19)	721 (2)	515 (1)	436 (4)
H(28)	C(20)	620 (2)	447 (1)	615 (3)

shown in Fig. 3. This is the first case of *cis* sarcosine for a linear oligopeptide in the crystalline state, although there have been several reports of *cis* peptide bonds in

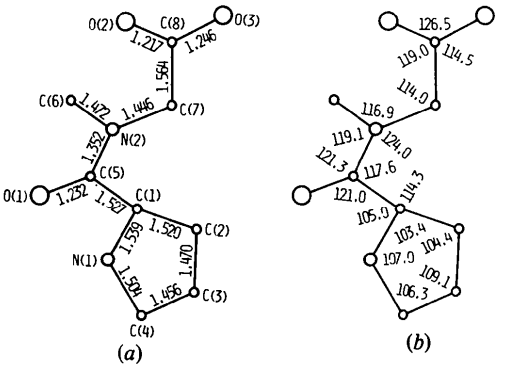


Fig. 1. (*a*) Bond lengths (Å), and (*b*) angles (°) for L-Pro-Sar.

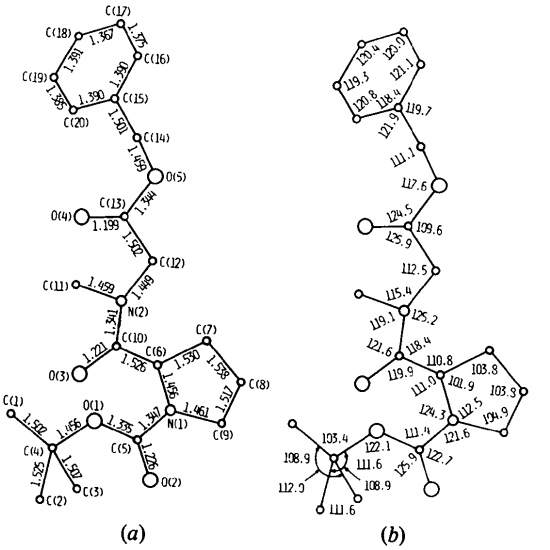


Fig. 2. (*a*) Bond lengths (Å), and (*b*) angles (°) for Boc-L-Pro-Sar-OBz.

solution. It is also interesting that the peptide bond in Boc-L-Pro-Sar (Itoh *et al.*, 1978) is *trans*.

The torsion angles (ω,φ,ψ) of *cis*-sarcosyl residues are listed in Table 6, together with those of *cis*-sarcosyl residues in several cyclic peptides. The standard deviations of (ω,φ,ψ) for this work are (0·8, 0·6, 0·5°) for L-Pro-Sar, and (0·5, 0·4, 0·3°) for Boc-L-Pro-Sar-OBz, respectively. It is evident that ω is significantly different from the ideal value (0°) and that φ(Sar) is distributed over a wider range than ψ(Pro) which is around $-65 \pm 10°$ in *trans* or *cis* peptides. The torsion angles in the present peptides agree well with those in the cyclic peptides, their mean values being (−5·6, −87·5, 175·4°). A weak correlation between ω and φ is observed: as the absolute value of ω increases, the absolute value of φ decreases.

In Fig. 4 the bond angles around the C′ and N atoms of the peptide bond are compared with the mean values for the peptides studied so far. The bond angles of the

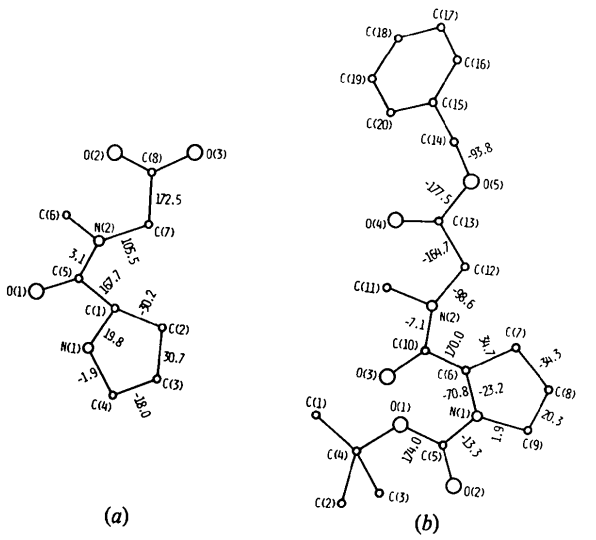


Fig. 3. Torsion angles (°) for (*a*) L-Pro-Sar, and (*b*) Boc-L-Pro-Sar-OBz.

Table 4. L-Pro-Sar: *equations of the best planes and displacements* ($\times 10^3$ Å) *of atoms from the planes* ($X = ax$, $Y = by$, $Z = cz$)

(I)	$-0{\cdot}8353X + 0{\cdot}1316Y - 0{\cdot}5338Z = -0{\cdot}7149$	Pro ring
(II)	$0{\cdot}3389X - 0{\cdot}6682Y + 0{\cdot}6624Z = -3{\cdot}8394$	Pro-Sar peptide
(III)	$-0{\cdot}1756X - 0{\cdot}8872Y - 0{\cdot}4267Z = -11{\cdot}3132$	Sar carboxyl

(I)		(II)		(III)	
C(1)	0 (46)	C(1)	−13 (23)	C(7)	−1 (11)
C(4)	0 (46)	C(5)	3 (23)	C(8)	4 (12)
N(1)	0 (46)	C(6)	−10 (23)	O(2)	−1 (11)
C(2)*	−502 (46)	C(7)	22 (23)	O(3)	−1 (11)
C(3)*	−46 (46)	N(2)	−13 (23)	N(2)*	−168 (11)
C(5)*	−950 (46)	O(1)	9·23)		

Dihedral angles (°) between the planes

(I)–(II) 43·6 (4) (II)–(III) 75·5 (2)

* Atoms not included in the calculation of the plane.

cis/trans form of the linear peptide agree approximately with those of the cyclic peptides. However, the bond angles around the N atoms of the sarcosyl residues depend strongly on the configuration, *cis* or *trans*, of the peptide bond. In the *cis* form, the angle C′—N—C^{α} is larger and C′—N—C^{Me} is smaller, both by about 6°, than those in the *trans* form. These differences seem to be caused by the bulky *N*-methyl group.

The role of the *N*-methyl group on the peptide structure is very similar to that of the prolyl side chain, though the sarcosyl residue has greater flexibility than the prolyl residue.

As shown in Fig. 3, the conformations of the peptide chains in the two molecules are similar, but the

Table 5. Boc-L-Pro-Sar-OBz: *equations of the best planes and displacements* ($\times 10^3$ Å) *of atoms from the planes* ($X = ax$, $Y = by$, $Z = cz$)

(I)	$-0{\cdot}2294X + 0{\cdot}4059Y - 0{\cdot}8635Z = -5{\cdot}7816$	Boc-Pro amide
(II)	$-0{\cdot}1665X - 0{\cdot}8679Y - 0{\cdot}4681Z = -7{\cdot}7835$	Pro-Sar peptide
(III)	$0{\cdot}1638X + 0{\cdot}3212Y - 0{\cdot}9327Z = -3{\cdot}3876$	Sar-OBz ester
(IV)	$-0{\cdot}2219X - 0{\cdot}6867Y - 0{\cdot}6922Z = -11{\cdot}2785$	Phenyl ring
(V)	$-0{\cdot}3814X + 0{\cdot}5082Y - 0{\cdot}7722Z = -4{\cdot}7403$	Pro ring

(I)		(II)		(III)	
C(5)	−6 (11)	C(6)	22 (7)	C(12)	1 (22)
C(6)	108 (11)	C(10)	−10(7)	C(13)	−2 (22)
C(9)	−24 (11)	C(11)	15 (7)	O(4)	1 (21)
N(1)	−79 (11)	C(12)	−41 (7)	O(5)	0 (21)
O(1)	−27 (11)	N(2)	32 (6)	C(14)*	−59 (22)
O(2)	47 (11)	O(3)	−15 (6)	N(2)*	352 (21)

(IV)		(V)	
C(15)	−2 (14)	C(6)	0 (41)
C(16)	7 (14)	C(9)	0 (41)
C(17)	−7 (14)	N(1)	0 (41)
C(18)	−1 (14)	C(7)*	−589 (41)
C(19)	8 (14)	C(8)*	−48 (41)
C(20)	−4 (14)	C(5)*	276 (41)
C(14)*	−52 (14)	C(10)*	1420 (41)

Dihedral angles (°) between the planes

(I)–(V)	9·2 (3)	(I)–(II)	84·2 (1)
(II)–(III)	82·5 (1)	(III)–(IV)	67·1 (2)

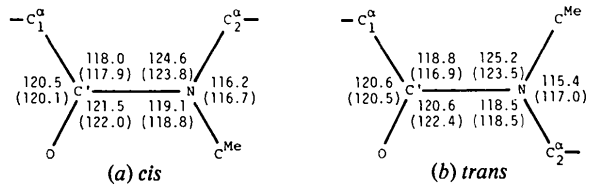
* Atoms not included in the calculation of the plane.

Table 6. *Torsion angles* (°) *of the cis-sarcosyl residues*

The enantiomorphs with negative φ are listed.

	Reference	ω	φ	ψ
L-Pro-Sar	1	−3·1	−105·5	−172·5
Boc-L-Pro-Sar-OBz	1	−7·1	−98·6	−164·7
cyclo(Gly-Sar-Gly-Sar)	2	−6·7	−84·8	166·2
cyclo[Gly-$(Sar)_3$]	2	1·9	−90·7	171·0
		7·2	−94·1	164·5
cyclo[DL-Ala-$(Sar)_3$]*A*	2	1·4	−91·2	165·6
		5·5	−91·3	158·7
cyclo[DL-Ala-$(Sar)_3$] *B*	2	−3·0	−85·1	162·3
		−6·1	−82·9	164·8
cyclo$(Sar)_4$	3	5·4	−93·6	169·5
cyclo$(Sar)_5$	4	−1·1	−102·0	173·4
		9·1	−89·1	176·2
		−14·1	−68·6	171·9
cyclo[L-Ala-$(Sar)_4$]	5	−4·9	−87·9	172·5
		5·3	−125·5	175·9
		−14·4	−68·1	170·8
cyclo$(Sar)_7$	6	−1·4	−86·7	−179·9
		−8·6	−92·4	−163·5
		−9·5	−82·0	179·6
		−13·2	−72·1	177·1
cyclo$(Sar)_8$	7	−1·0	−106·9	179·8
		−5·6	−91·9	−173·4
		−9·0	−77·5	−167·5
		−15·8	−72·3	−167·0
Actinomycin D	8	−1·2	−76·7	−175·2

References: (1) This study; (2) Declercq *et al.* (1975); (3) Groth (1970); (4) Groth (1973*b*); (5) Groth (1974); (6) Groth (1975); (7) Groth (1973*a*); (8) Jain & Sobell (1972).



(*a*) *cis* (*b*) *trans*

Fig. 4. Bond angles (°) around the C′ and N atoms of the peptide bond. (*a*) *cis* form, upper values: present peptides (mean values); lower: mean values for the cyclic peptides. (*b*) *trans* form, upper: Boc-L-Pro-Sar; lower: mean values of the cyclic peptides.

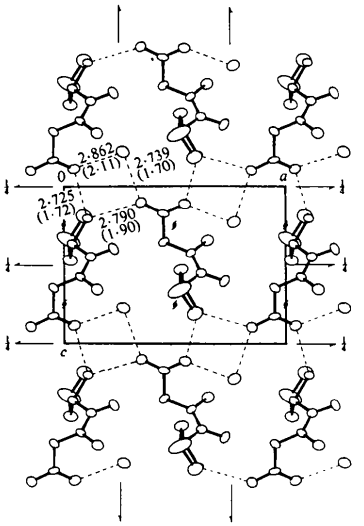


Fig. 5. Crystal structure of L-Pro-Sar. Hydrogen bonds are shown as dashed lines.

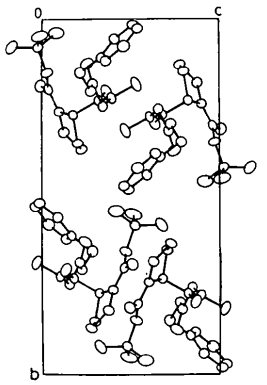


Fig. 6. Crystal structure of Boc-L-Pro-Sar-OBz.

conformations of the pyrrolidine rings are quite different. The ring in L-Pro-Sar is C_s-C^{β}-*endo*, and that in Boc-L-Pro-Sar-OBz is C_s-C^{β}-*exo* (Ashida & Kakudo, 1974).

Molecular packing

The molecular-packing arrangements of the two peptides are shown in Figs. 5 and 6. The hydrogen bonds in L-Pro-Sar are listed in Table 7. The crystal structure of L-Pro-Sar is stabilized by a hydrogen-bond network. All of the four available H atoms per molecule are utilized in forming the hydrogen bonds, in which the water molecule acts as donor. In contrast, the packing of Boc-L-Pro-Sar-OBz is determined only by van der Waals interactions, and no significant short intermolecular contacts are observed.

Table 7. *Hydrogen bonds in* L-Pro-Sar

Donor	Acceptor	Distances (Å)		Angle (°)
D–H	*A*	*D*···*A*	H···*A*	*D*–H···*A*
O(*W*)	O(2)^{I}	2·862 (8)	2·11 (6)	162 (6)
O(*W*)	O(3)^{II}	2·725 (8)	1·72 (7)	176 (6)
N(1)	O(2)^{III}	2·739 (6)	1·70 (6)	175 (5)
N(1)	O(3)^{IV}	2·790 (6)	1·99 (6)	152 (6)

Symmetry code

(I) x, y, z (III) $x, y, -1+z$
(II) $\frac{1}{2}+x, \frac{3}{2}-y, 2-z$ (IV) $\frac{1}{2}+x, \frac{3}{2}-y, 1-z$

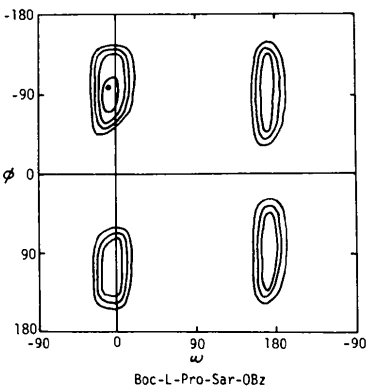


Fig. 7. The ω–φ energy map for Boc-L-Pro-Sar-OBz. The contours are at intervals of −10 kcal (≡ −42 kJ)/residue starting at 50 kcal (≡ 210 kJ)/residue. The location of the global energy minimum is shown by a dot.

Conformational stability

It is interesting that the conformations of the main chains of these peptides agree well with each other, though the packing schemes in the crystal clearly differ. This suggests that the *cis* configuration in the sarcosyl residue is as stable as the *trans*.

For the L-Pro-Sar sequence, present in the linear oligopeptides L-Pro-Sar, Boc-L-Pro-Sar and Boc-L-Pro-Sar-OBz, the conformational energies were calculated over the whole range of ω and φ(Sar), but φ(Pro), ψ(Pro) and ψ(Sar) were held fixed. The geometry of each residue was adopted from the present structure analysis. The total energy was calculated as a sum of torsional, electrostatic and van der Waals energies according to the method of Ooi, Scott, Vanderkooi &

Sheraga (1967). The ω–φ energy maps of the three cases showed results approximately similar to one another; the ω–φ energy map of Boc-L-Pro-Sar-OBz is shown in Fig. 7. There exist four minimum-energy regions in each of the conformational maps of the three peptides. The differences between the energy minima in the four regions are not significant. Thus, the conformational-energy calculation, although it requires further refinement, shows that for the sarcosyl residue the *cis* peptide bond is able to exist with the same energetical stability as the *trans* peptide bond. The configuration may be mainly determined by the intramolecular interactions with other groups in the molecule and intermolecular forces.

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The Structure of *tert*-Butoxycarbonyl-L-prolyl-L-isoleucylglycine

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Abstract

The crystal structure of the title compound was determined by the X-ray method. The space group is $P2_12_12$ with $a = 12{\cdot}909$ (1), $b = 17{\cdot}567$ (2), $c = 10{\cdot}055$ (3) Å and $Z = 4$. The structure was solved by a direct method. In contrast to the β-turn conformation of a similar sequential peptide Boc-Pro-Leu-Gly-OH, this compound takes an extended conformation to form a dimer structure *via* β-sheet-type hydrogen bonds. The disordered water on the twofold axis only plays a role as a hydrogen donor.

Introduction

Among the tripeptides of *N*-(*tert*-butoxycarbonyl)-Pro-*X*-Gly-OH (Boc-Pro-*X*-Gly-OH; *X*: any amino acid residue) type, two compounds, Boc-Pro-Pro-Gly-OH (Hudson, Shaw, Schurr & Jensen, 1972) and Boc-Pro-Leu-Gly-OH (Ashida, Tanaka, Shimonishi & Kakudo, 1977), were studied by the X-ray method, and in the crystalline state an extended conformation was found for the former and a folded or so-called β-turn conformation for the latter. This structural difference is reasonable in view of the structural role of the prolyl and leucyl residues. The prolyl residue is not expected to be accommodated at the third site of the β-turn.

The β-turn conformation is considered to be one of the most important secondary structures in the globular proteins, since it gives a protein its globularity rather than linearity (Chou & Fasman, 1977). Therefore, several peptides of Boc-Pro-*X*-Gly-OH (*X*: Ile, Ala, Val, Met, Phe, *etc.*) were prepared in an attempt to study the effects of various side chains of *X* on the peptide conformations. The present analysis was performed for Boc-Pro-Ile-Gly-OH. Since a forked side

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