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tert-Butyloxycarbonylsarcosylglycine Benzyl Ester

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Abstract. $C_{17}H_{24}N_2O_5$, monoclinic, $P2_1/c$; $a=12{\cdot}503\,(2)$, $b=6{\cdot}312\ (2)$, $c=24{\cdot}380\ (5)$ Å, $\beta=102{\cdot}55\ (2)°$; $M=336{\cdot}38$, $Z=4$, $D_m=1{\cdot}19$, $D_x=1{\cdot}190$ g cm^{-3}; μ(Cu $K\alpha$) $=6{\cdot}88$ cm^{-1}; $R=0{\cdot}050$ for 2691 reflexions. The linkage between the *tert*-butyloxycarbonyl group and the sarcosyl residue is *cis*. The (φ,ψ) angles of the sarcosyl residue, (72·3, −153·7°), essentially agree with those of the *cis* sarcosyl residue in the cyclic peptides.

Introduction. $C_{17}H_{24}N_2O_5$ was prepared and crystallized by Sugihara, Imanishi & Higashimura (1975). The intensity data were collected on a Rigaku automatic four-circle diffractometer (AFC-IV, at the Institute for Protein Research, Osaka University), using the ω–2θ scan method. Ni-filtered Cu $K\alpha$ radiation (40kV, 200mA) was used. A crystal of dimensions $0{\cdot}4\times0{\cdot}3\times0{\cdot}3$mm was selected. 2691 independent reflexions with $2\theta\leq118°$ were obtained, of which 2617 were non-zero. The intensity data were corrected for Lorentz and polarization effects, but an absorption correction was not made.

The structure was solved by the use of *MULTAN* (Germain, Main & Woolfson, 1970). On the *E* map calculated from the best set of the phase angles, 21 of the 24 non-hydrogen atoms were located. Difference Fourier syntheses revealed the three remaining C atoms. The refinement was carried out by the block-diagonal least-squares method with *HBLS* (Ashida, 1973). All the H atoms were obtained on a difference map, and were included in the refinement. The *R* value was reduced to 0·050 for all the 2691 reflexions. The weighting scheme was: $\omega=\frac{1}{2}$ for $|F_o|=0$, $\omega=1$ for $|F_o|\leq25$ and $\omega=(25/|F_o|)^2$ for $|F_o|>25$. The atomic scattering factors of the C, N and O atoms were taken from *International Tables for X-ray Crystallography* (1962) and that of the H atom from *International Tables for X-ray*

Table 1. *Positional* ($\times10^4$) *and thermal* ($\times10^4$) *parameters, with their standard deviations in parentheses*

The temperature factor is of the form: $\exp[-(\beta_{11}h^2+\beta_{22}k^2+\beta_{33}l^2+\beta_{12}hk+\beta_{13}hl+\beta_{23}kl)]$.

	x	y	z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
C(1)	−175 (3)	−6355 (7)	−897 (2)	109 (3)	740 (18)	57 (2)	−60 (12)	60 (3)	120 (8)
C(2)	−281 (3)	−2864 (7)	−1386 (2)	85 (3)	556 (14)	74 (2)	160 (10)	28 (3)	79 (8)
C(3)	137 (3)	−6144 (7)	−1880 (2)	118 (3)	734 (17)	35 (1)	−101 (12)	−33 (3)	−22 (7)
C(4)	247 (2)	−5053 (5)	−1317 (2)	59 (2)	422 (10)	37 (1)	−19 (7)	11 (2)	24 (5)
C(5)	2187 (2)	−6001 (4)	−978 (1)	71 (2)	245 (7)	16 (1)	2 (6)	12 (2)	−2 (3)
C(6)	4127 (2)	−6469 (5)	−634 (1)	68 (2)	376 (9)	28 (1)	65 (7)	11 (2)	5 (4)
C(7)	3256 (2)	−2883 (4)	−623 (1)	75 (2)	248 (7)	17 (1)	−41 (6)	18 (2)	−9 (3)
C(8)	2901 (2)	−2460 (4)	−75 (1)	63 (2)	268 (7)	17 (1)	−34 (6)	13 (2)	−5 (3)
C(9)	2363 (2)	434 (5)	473 (1)	82 (2)	364 (9)	23 (1)	−18 (7)	28 (2)	−49 (4)
C(10)	3412 (2)	1220 (4)	845 (1)	80 (2)	260 (7)	20 (1)	1 (6)	28 (2)	−4 (3)
C(11)	4129 (2)	3129 (6)	1679 (2)	79 (2)	572 (12)	26 (1)	−52 (8)	17 (2)	−98 (5)
C(12)	3679 (2)	4623 (4)	2051 (1)	77 (2)	357 (8)	18 (1)	−68 (7)	12 (2)	−31 (3)
C(13)	3539 (3)	3975 (5)	2572 (1)	139 (3)	349 (9)	19 (1)	−51 (8)	17 (2)	−5 (4)
C(14)	3096 (3)	5353 (6)	2905 (1)	160 (4)	489 (11)	18 (1)	−79 (10)	35 (2)	−29 (4)
C(15)	2811 (3)	7358 (5)	2725 (2)	110 (3)	431 (10)	26 (1)	−19 (8)	21 (2)	−68 (4)
C(16)	2952 (3)	8008 (5)	2209 (2)	128 (3)	338 (9)	32 (1)	3 (9)	15 (3)	−9 (4)
C(17)	3379 (3)	6637 (5)	1876 (1)	117 (3)	404 (10)	22 (1)	−58 (8)	28 (2)	14 (4)
N(1)	3171 (2)	−5100 (3)	−786 (1)	61 (2)	242 (5)	19 (1)	10 (4)	12 (1)	−11 (3)
N(2)	2541 (2)	−475 (3)	−42 (1)	102 (2)	271 (6)	18 (1)	15 (5)	20 (2)	−13 (3)
O(1)	1406 (2)	−4523 (3)	−1094 (1)	61 (1)	248 (5)	29 (1)	8 (4)	5 (1)	0 (3)
O(2)	2039 (2)	−7896 (3)	−1047 (1)	99 (2)	209 (5)	25 (1)	−8 (4)	5 (1)	−14 (2)
O(3)	2971 (2)	−3762 (3)	297 (1)	122 (2)	343 (6)	21 (1)	51 (5)	40 (2)	45 (3)
O(4)	4308 (2)	1002 (3)	761 (1)	75 (2)	474 (7)	30 (1)	−33 (5)	43 (2)	−62 (3)
O(5)	3186 (2)	2218 (3)	1290 (1)	72 (2)	384 (6)	20 (1)	−32 (4)	25 (1)	−49 (2)

Crystallography (1974). All the calculations were carried out on a FACOM 230-60 computer at the Computer Centre of Nagoya University. The final atomic parameters are listed in Tables 1 and 2.*

* A list of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 31932 (12 pp., 1 microfiche). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 2. *Positional* ($\times 10^3$) *and thermal* ($\times 10$) *parameters of hydrogen atoms*

Standard deviations are given in parentheses.

	Bonded to	x	y	z	B
H(1)	C(1)	14 (3)	−582 (6)	−49 (2)	90 (11)
H(2)	C(1)	−99 (4)	−648 (7)	−103 (2)	109 (12)
H(3)	C(1)	18 (3)	−765 (6)	−80 (2)	87 (10)
H(4)	C(2)	2 (3)	−208 (6)	−162 (2)	91 (10)
H(5)	C(2)	−18 (4)	−249 (8)	−96 (2)	113 (13)
H(6)	C(2)	−111 (4)	−300 (7)	−154 (2)	112 (13)
H(7)	C(3)	51 (4)	−539 (8)	−211 (2)	123 (14)
H(8)	C(3)	−76 (4)	−636 (7)	−201 (2)	109 (12)
H(9)	C(3)	52 (4)	−757 (8)	−185 (2)	112 (13)
H(10)	C(6)	476 (2)	−564 (4)	−63 (1)	43 (6)
H(11)	C(6)	415 (3)	−756 (6)	−92 (2)	86 (10)
H(12)	C(6)	422 (3)	−703 (5)	−26 (2)	56 (7)
H(13)	C(7)	282 (2)	−206 (4)	−93 (1)	31 (5)
H(14)	C(7)	409 (2)	−253 (5)	−55 (1)	43 (6)
H(15)	C(9)	202 (2)	−59 (4)	67 (1)	41 (6)
H(16)	C(9)	182 (2)	163 (5)	39 (1)	48 (7)
H(17)	C(11)	466 (3)	379 (5)	144 (2)	69 (8)
H(18)	C(11)	458 (3)	194 (6)	190 (2)	77 (9)
H(19)	C(13)	377 (3)	254 (6)	270 (2)	67 (8)
H(20)	C(14)	301 (3)	484 (6)	326 (2)	81 (10)
H(21)	C(15)	242 (3)	836 (6)	296 (2)	86 (10)
H(22)	C(16)	261 (3)	938 (6)	288 (2)	79 (9)
H(23)	C(17)	352 (3)	702 (6)	150 (2)	72 (9)
H(24)	N(2)	243 (2)	32 (5)	−32 (1)	42 (6)

Discussion. The bond distances, angles and torsion angles of the peptide main chain are shown in Fig. 1, together with the numbering of atoms in the molecule. The mean e.s.d.'s of the bond distances and angles are 0·004 Å and 0·3°. The definition of the torsion angles given by the IUPAC–IUB Commission on Biochemical Nomenclature (1970) is adopted. The equations of the best planes of several planar groups and the displacements of atoms from the planes are listed in Table 3. Two amide groups are not planar, but significantly twisted. An *ORTEP* (Johnson, 1965) drawing of the molecule is shown in Fig. 2.

The linkage between the *tert*-butyloxycarbonyl group and the sarcosyl residue has a *cis* conformation; that is, the dihedral angle between the planes O(1)N(1)-C(5) and N(1)C(5)C(7) is 12·5°. The linkage between the *tert*-butyloxycarbonyl or *tert*-amyloxycarbonyl group and the *N*-terminal prolyl residue is *cis* in every peptide whose structure has been determined (Matsuzaki, 1974; Benedetti, Ciajolo & Maisto, 1974; Kartha, Ashida & Kakudo, 1974). In *N-tert*-butyloxycarbonyl-*S*-benzylcysteinylglycine methyl ester (Kashino, Ashida & Kakudo, 1974) the corresponding linkage is *trans*. The *cis* conformation of this linkage seems to be a common feature of the *N*-substituted amino acid residue.

The (φ, ψ) pairs of the sarcosyl residues in several peptides so far reported are compared in Table 4. Four of the five structures have a *cis* peptide linkage. Further it should be noted that all of these residues have essentially the same (φ, ψ) pair. The rotation angle φ of the N–C$^\alpha$ bond is largely restricted by the methyl group substituted at the N atom. The (ω, φ, ψ) angles of the other enantiomer of these residues are fairly close to those (0, −83, 158°) of the prolyl res-

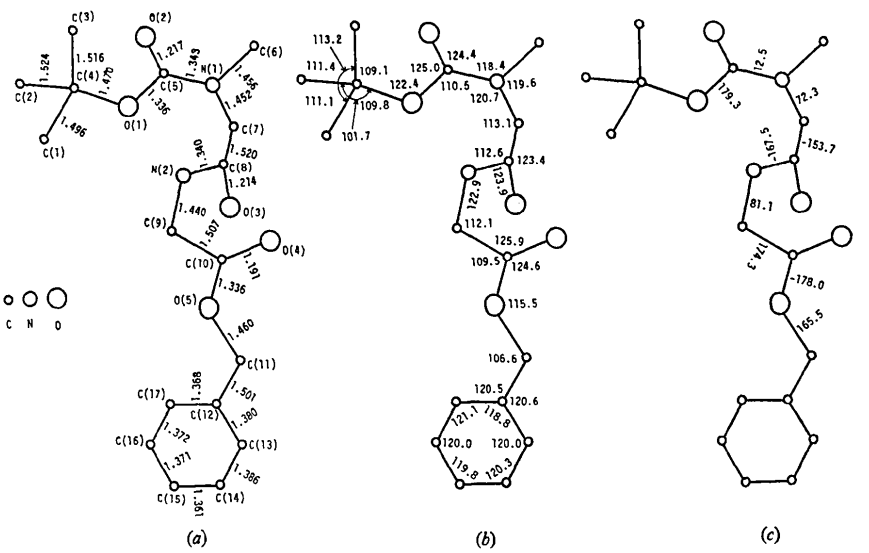

Fig. 1. (*a*) Bond distances, (*b*) bond angles and (*c*) torsion angles of the peptide main chain. The definition given by the IUPAC–IUB Commission on Biochemical Nomenclature (1970) is adopted.

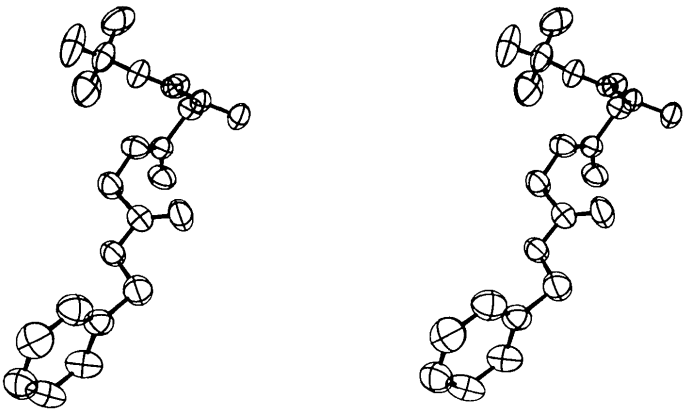

Fig. 2. Stereo drawing of the molecule with thermal ellipsoids drawn to enclose 50% probability.

Table 3. *Best planes*

(*a*) Equations of the best planes
$X = ax + cz\cos\beta$, $Y = by$, $Z = cz\sin\beta$

(I) Amide Boc–Sar:
$-0{\cdot}3682X - 0{\cdot}1349Y + 0{\cdot}9199Z + 2{\cdot}8279 = 0$

(II) Peptide Sar–Gly:
$-0{\cdot}8900X - 0{\cdot}2550Y - 0{\cdot}3780Z + 2{\cdot}8320 = 0$

(III) Ester Gly–OBzl:
$0{\cdot}0155X + 0{\cdot}8630Y - 0{\cdot}5050Z + 0{\cdot}2908 = 0$

(IV) Benzene ring:
$-0{\cdot}8496X - 0{\cdot}3217Y - 0{\cdot}4181Z + 5{\cdot}9630 = 0$

(*b*) Dihedral angles (°) between the planes

	(I)	(II)	(III)
(II)	89·2		
(III)	125·9	92·5	
(IV)	91·6	5·0	94·6

(*c*) Displacements ($\times 10^3$ Å) of atoms from the planes

(I)		(II)		(III)		(IV)	
C(5)	0	C(7)	−60	C(9)	0	C(12)	−1
C(6)	−32	C(8)	32	C(10)	−1	C(13)	−4
C(7)	89	C(9)	−70	O(4)	0	C(14)	5
N(1)	−72	N(2)	99	O(5)	0	C(15)	−2
O(1)	−43	O(3)	5	C(11)*	45	C(16)	−3
O(2)	66	C(10)*	−1522	N(2)*	132	C(17)	4
C(4)*	4	N(1)*	461			C(11)*	28
C(8)*	1522	H(24)*	214			H(19)*	−26
						H(20)*	3
						H(21)*	78
						H(22)*	149
						H(23)*	−20

* Not included in the calculation of the best planes.

Table 4. *Torsion angles of sarcosyl residues in peptides*

	ω (°)*	φ (°)	ψ (°)
Present peptide	12·5	72·3	−153·7
Actinomycin D[a]	−0·1	80·0	−169·5
	2·5	73·3	179·1
Cyclotetrasarcosyl[b]	−5·4	93·6	−169·5
	−170·6	120·8	−65·5

(*a*) Jain & Sobell (1972). (*b*) Groth (1970).

* Torsion angle about the amide C′–N bond in X–Sar, where X is the *tert*-butyloxycarbonyl group or an amino acid residue.

idues in poly(L-proline) (Ramachandran & Sasisekharan, 1968).

There is only one hydrogen bond between N(2) and O(2) $(x, 1+y, z)$. Its distances and angle are: N(2)···O(2) 2·895, H(24)···O(2) 2·06 Å and N(2)–H(24)···O(2) 175°. Some of the other intermolecular distances, neglecting H atoms, are: C(7)···O(4) $(1-x, -y, -z)$ 3·353, C(5)···N(2) $(x, -1+y, z)$ 3·598 and O(3)···O(5) $(x, -1+y, z)$ 3·476 Å.

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