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N-t-Butyloxycarbonyl-*S*-benzylcysteinylglycine Methyl Ester

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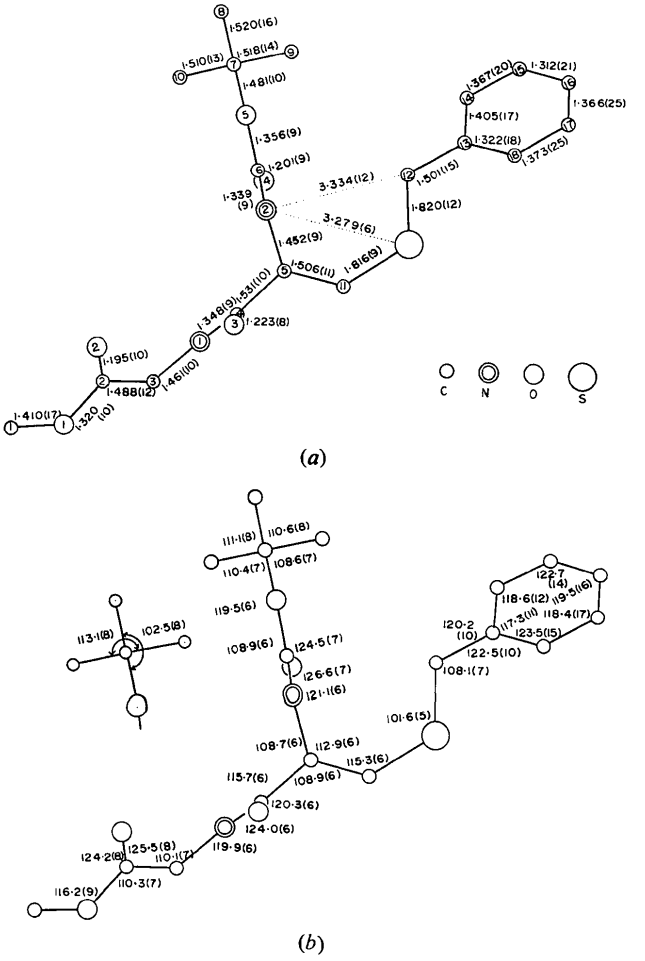
Abstract.
$(CH_3)_3COCONHCH(CH_2SCH_2C_6H_5)CONHCOOCH_3$ monoclinic, space group $P2_1$, $a=16{\cdot}970$ (2), $b=5{\cdot}022$ (1), $c=12{\cdot}142$ (1) Å, and $\beta=96{\cdot}99$ (1)°. $\varrho_{obs}=1{\cdot}21$, $\varrho_{calc}=1{\cdot}24$ g cm^{-3}, $Z=2$. The structure was refined to $R=0{\cdot}064$ for 1517 observed reflexions. The dihedral angle between the two peptide planes is 116·1° and the internal rotation angles φ, ψ and ω in the peptide backbone are −124·0, 103·2 and 179·7°, respectively. The molecules are joined together through N–H···O hydrogen bonds (2·915 (8) and 3·024 (7) Å) in the **b** direction to form a parallel-chain pleated sheet.

Introduction. The material was kindly supplied by Tanabe Seiyaku Co. Ltd., Osaka. The crystals obtained by slow evaporation from ethanol and water solution were needles elongated along the *b* axis. The systematic absence was $0k0$, k odd. Lattice constants and intensities were measured from a crystal of dimensions $0{\cdot}06\times0{\cdot}30\times0{\cdot}07$ mm, on an automatic four-circle diffractometer with Ni-filtered Cu $K\alpha$ radiation using a scintillation counter with pulse-height analyser. The $\omega/2\theta$-scan method was employed (scan speed: 4° min^{-1}; scan range in 2θ: $1{\cdot}0+0{\cdot}15\tan\theta_B$, where θ_B is Bragg angle). Background was measured for 10 s on either side of the peak. In total 1732 independent reflexions were surveyed up to $2\theta=120°$, and 1517 non-zero reflexions were obtained. Corrections for Lorentz and polarization effects were applied, but no absorption correction was made [μ(Cu $K\alpha$) = 16·1 cm^{-1}].

The parameters of the sulphur atom were found in the Patterson map sharpened with $B=4{\cdot}4$ Å^2. The minimum-function map calculated on the basis of these parameters revealed 23 non-hydrogen atoms (program *MFPA*, Tanaka & Yasuoka, 1973). These atoms were included in block-diagonal least-squares calculation followed by Fourier summation (*HBLS*-5, Ashida, 1973), from which the positions of all non-hydrogen atoms were obtained. The least-squares refinement including these atoms with anisotropic thermal parameters resulted in $R=0{\cdot}106$. The hydrogen atoms were found on the difference electron density map, and were included in the subsequent refinements. The weights adopted in the later stages of the refinement were: $w=[\sigma(F_o)^2+0{\cdot}01755|F_o|+0{\cdot}00063|F_o|^2]^{-1}$. The final R value is 0·064 for 1517 observed reflexions. The atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1962). The computations were performed on the NEAC 2200-700 computer in the Computation Center of Osaka University.

The final atomic parameters are listed in Tables 1 and 2.† The molecular structure viewed along the *b* axis is shown in Fig. 1 along with bond lengths and angles.

† A table of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 30501 (10 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.



(*a*)

(*b*)

Fig. 1. The molecular structure: (*a*) bond lengths (Å) and numbering of atoms, (*b*) bond angles (°). Their estimated standard deviations are shown in parentheses.

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Discussion. Most of the oligopeptides studied by X-ray analysis have two terminal hydrophilic groups, $-NH_3^+$ and $-CO_2^-$, which might cause some distortion of the molecular conformation and intermolecular N–H···O hydrogen bonds. However, in the present compound such terminal groups are masked with hydrophobic residues. A study of the structure is therefore of significance with regard to the structural chemistry of oligopeptides and proteins.

The C–S bond lengths and the C–S–C bond angle are in agreement with the corresponding values found in glutathione (1·78 Å, Wright, 1958), α- and β-methionine (1·77, 1·79 Å, 100°; 1·78, 1·80 Å, 100°, Mathieson, 1952), and L-methionine [1·832 (15), 1·805 (27) Å, 99·8 (1·0)°; 1·792 (26), 1·718 (31) Å, 101·8 (1·4)°, Torii & Iitaka, 1973]. The average C–C bond length in the benzene ring, 1·358 (21) Å, is shorter than the normal value. This is probably due to the large thermal vibrations of the ring. The bond lengths and angles for the peptide group are in agreement with the standard values (Corey & Pauling, 1953). The dihedral angle between the two peptide planes is 116·1°. The internal rotation angles (defined by the IUPAC-IUB Commission on Biochemical Nomenclature, 1970) φ, ψ and ω in the peptide backbone are −124·0, 103·2 and 179·7° respectively. The distance between the C(3) and O(5) atoms is 6·28 Å. These values are very close to those proposed for the parallel-chain pleated-sheet structure (Pauling & Corey, 1953). Such β-type structures in the crystals of oligopeptides have been found in glycylphenylalanylglycine (GPG) (Marsh & Glusker, 1961) and DL-acetylleucine-*N*-methylamide (ALNMA) (Ichikawa & Iitaka, 1969).

Table 2. *The final parameters of the hydrogen atoms*

	x	*y*	*z*	*B*(Å²)	Bonded to
H(1)	−0·158	−0·211	−0·623	9·3	C(1)
H(2)	−0·098	−0·365	−0·606	5·3	C(1)
H(3)	−0·186	−0·440	−0·554	4·6	C(1)
H(4)	−0·109	0·054	−0·286	0·7	C(3)
H(5)	−0·042	0·214	−0·342	3·1	C(3)
H(6)	0·024	−0·279	−0·222	1·5	N(1)
H(7)	0·103	−0·187	−0·077	0·7	C(5)
H(8)	0·198	0·245	−0·133	0·5	N(2)
H(9)	0·478	−0·137	−0·218	6·7	C(8)
H(10)	0·426	0·112	−0·268	7·6	C(8)
H(11)	0·450	0·039	−0·118	5·4	C(8)
H(12)	0·405	−0·234	−0·022	7·9	C(9)
H(13)	0·355	−0·547	−0·045	6·8	C(9)
H(14)	0·438	−0·528	−0·094	6·1	C(9)
H(15)	0·322	−0·280	−0·330	6·9	C(10)
H(16)	0·386	−0·463	−0·310	5·3	C(10)
H(17)	0·311	−0·554	−0·261	7·5	C(10)
H(18)	0·055	0·113	0·046	3·5	C(11)
H(19)	0·121	0·336	0·035	1·7	C(11)
H(20)	0·231	0·436	0·132	5·2	C(12)
H(21)	0·280	0·189	0·076	2·1	C(12)
H(22)	0·377	−0·119	0·171	5·7	C(14)
H(23)	0·453	−0·269	0·334	6·4	C(15)
H(24)	0·441	−0·046	0·509	7·0	C(16)
H(25)	0·351	0·280	0·489	9·1	C(17)
H(26)	0·274	0·430	0·338	6·5	C(18)

$\langle\sigma(x)\rangle = 0{\cdot}063$, $\langle\sigma(y)\rangle = 0{\cdot}094$, $\langle\sigma(z)\rangle = 0{\cdot}070$ Å $\langle\sigma(B)\rangle = 2{\cdot}0$ Å²

The internal rotation angles χ_1, χ_2, χ_3 and χ_4 defining the conformation of the side chain take the values of −65·4, 88·3, 169·5 and 91·1° respectively. The S atom in the γ position is situated in the *gauche* position with respect to the N(2) atom and *trans* to the C(4) atom. Similar conformation of the side chain is found in ALNMA, while in GPG the corresponding γ carbon

Table 1. *The final atomic coordinates and thermal parameters* ($\times 10^4$) *with standard deviations in parentheses*

The anisotropic coefficients have 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}
S	1704 (1)	0 (6)	1447 (1)	41 (1)	606 (10)	72 (1)	−54 (5)	−12 (1)	104 (8)
C(1)	−1450 (5)	−2744 (31)	−5767 (7)	62 (4)	1445 (98)	104 (7)	36 (39)	−43 (9)	−306 (52)
C(2)	−672 (4)	−1704 (16)	−4119 (5)	41 (3)	456 (35)	60 (5)	−10 (18)	−9 (6)	25 (24)
C(3)	−580 (4)	235 (17)	−3185 (5)	37 (2)	468 (36)	72 (5)	−40 (19)	−4 (5)	−33 (27)
C(4)	459 (3)	1184 (14)	−1675 (5)	26 (2)	315 (27)	64 (4)	6 (14)	13 (5)	39 (20)
C(5)	1112 (3)	67 (15)	−818 (5)	34 (2)	296 (28)	70 (4)	11 (17)	4 (5)	34 (24)
C(6)	2380 (4)	−1450 (14)	−1326 (5)	32 (2)	293 (27)	77 (5)	−56 (15)	12 (5)	6 (23)
C(7)	3717 (4)	−2248 (16)	−1824 (7)	37 (3)	306 (35)	170 (9)	39 (17)	32 (8)	−44 (31)
C(8)	4365 (5)	−331 (22)	−2076 (11)	58 (4)	425 (43)	344 (18)	22 (26)	176 (14)	−13 (56)
C(9)	3986 (5)	−3861 (21)	−789 (7)	50 (3)	742 (58)	133 (8)	95 (26)	11 (8)	−61 (39)
C(10)	3442 (5)	−3958 (20)	−2820 (7)	71 (4)	593 (51)	121 (8)	160 (26)	40 (9)	−43 (34)
C(11)	1042 (4)	1331 (16)	290 (5)	35 (2)	559 (39)	62 (5)	−71 (19)	−5 (5)	60 (25)
C(12)	2583(4)	2060 (23)	1404 (6)	45 (3)	897 (62)	98 (7)	−95 (26)	−17 (7)	196 (39)
C(13)	3136 (4)	1554 (19)	2445 (6)	36 (3)	670 (48)	85 (6)	−51 (21)	6 (6)	−41 (30)
C(14)	3719 (5)	−439 (28)	2467 (6)	55 (3)	1139 (76)	90 (6)	97 (34)	34 (7)	0 (45)
C(15)	4209 (5)	−854 (29)	3431 (8)	54 (4)	1213 (92)	137 (9)	153 (34)	−2 (9)	61 (50)
C(16)	4132 (5)	441 (32)	4351 (7)	61 (4)	1564 (112)	92 (7)	−140 (42)	−27 (8)	−31 (55)
C(17)	3564 (7)	2369 (39)	4349 (9)	107 (7)	1743 (132)	126 (9)	196 (58)	−33 (13)	−319 (67)
C(18)	3081 (6)	2854 (30)	3379 (8)	79 (5)	1221 (92)	130 (9)	190 (38)	−47 (11)	−291 (52)
N(1)	52 (3)	−630 (11)	−2336 (4)	33 (2)	321 (26)	68 (4)	21 (13)	−13 (4)	−3 (18)
N(2)	1876 (3)	553 (10)	−1205 (4)	29 (2)	271 (25)	87 (4)	31 (11)	20 (4)	41 (18)
O(1)	−1317 (3)	−1158 (14)	−4804 (4)	42 (2)	914 (41)	78 (4)	38 (16)	−29 (4)	−137 (22)
O(2)	−235 (3)	−3520 (12)	−4235 (4)	65 (2)	496 (26)	82 (4)	94 (15)	−12 (5)	−50 (19)
O(3)	329 (3)	3579 (10)	−1724 (4)	45 (2)	325 (20)	84 (4)	33 (11)	−22 (4)	−15 (17)
O(4)	2252 (3)	−3785 (10)	−1226 (5)	41 (2)	253 (20)	170 (6)	4 (12)	41 (5)	−13 (20)
O(5)	3074 (2)	−425 (10)	−1580 (4)	35 (2)	245 (20)	176 (6)	4 (11)	60 (5)	−21 (21)

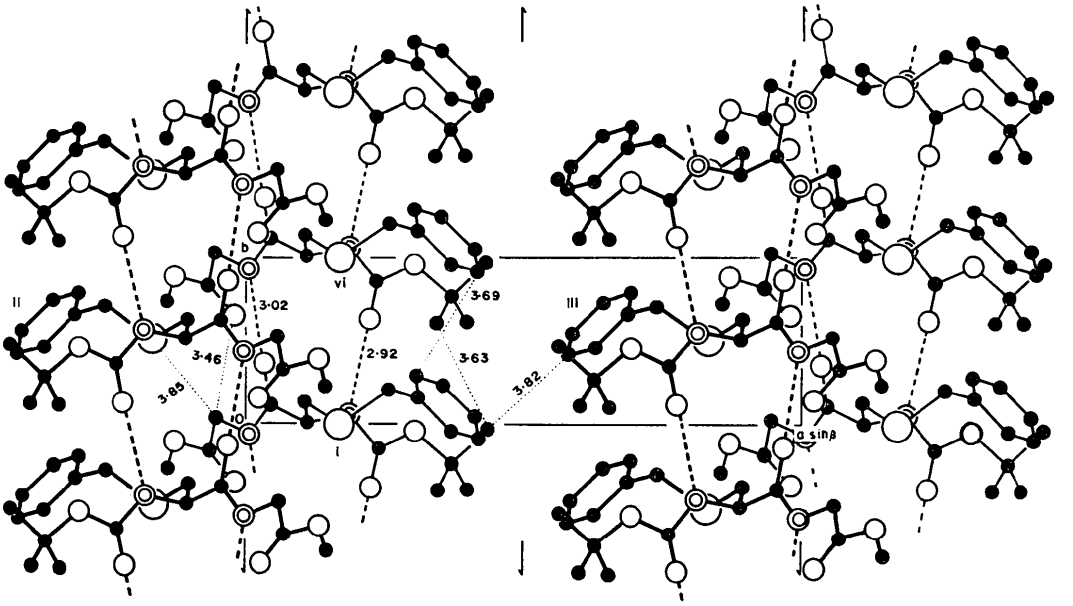

Fig. 2. The projection of the crystal structure viewed along the *c* axis. Broken lines show hydrogen bonds, and dotted lines intermolecular contacts. Symmetry code: i x,y,z; ii $-x,\frac{1}{2}+y,-z$; iii $1-x,\frac{1}{2}+y,-z$; iv $1-x,\frac{1}{2}+y,1-z$; v $x,y,1+z$; vi $x,1+y,z$.

atom is *trans* to the amide nitrogen atom. A slight widening of χ_1 from $-60°$ seems to result from the intramolecular repulsion between the N(2) and S atoms. In fact, both the bond angles C(5)–C(11)–S and N(2)–C(5)–C(11) are significantly larger than the regular tetrahedral angle.

The projection of the crystal structure along the *c* axis is shown in Fig. 2. The molecules are joined together in the **b** direction by two N–H···O hydrogen bonds [N(2)···O(4) = 2·915 (8) Å, N(2)–H(8)···O(4) = 168 (5)°; N(1)···O(3) = 3·024 (7) Å, N(1)–H(6)···O(3) = 163 (5)°] to form a parallel-chain pleated sheet. The distance between adjacent chains, 5·02 Å, corresponds to the proposed value, 4·85 Å (Pauling & Corey, 1953), and the observed one, 4·90 Å, in GPG. The *S*-benzyl side chain extends along [305], which is almost parallel to the long axis of the molecule and perpendicular to the chain containing the t-butyloxycarbonyl group. They form a hydrophobic region between adjacent sheets. The van der Waals forces between the hydrophobic groups play a key role in gathering the β-sheets together.

References

ASHIDA, T. (1973). *The Universal Crystallographic Computing System–Osaka*, pp. 55–61. The Computation Centre, Osaka Univ.

COREY, R. B. & PAULING, L. (1953). *Proc. Roy. Soc.* B**141**, 10–20.

ICHIKAWA, T. & IITAKA, Y. (1969). *Acta Cryst.* B**25**, 1824–1833.

International Tables for X-ray Crystallography (1962). Vol. III, pp. 202–203. Birmingham: Kynoch Press.

IUPAC-IUB COMMISSION ON BIOCHEMICAL NOMENCLATURE (1970). *J. Mol. Biol.* **52**, 1–17.

MARSH, R. E. & GLUSKER, J. P. (1961). *Acta Cryst.* **14**, 1110–1116.

MATHIESON, A. McL. (1952). *Acta Cryst.* **5**, 332–341.

PAULING, L. & COREY, R. B. (1953). *Proc. Natl. Acad. Sci. U.S.* **39**, 253–256.

TANAKA, N. & YASUOKA, N. (1973). *The Universal Crystallographic Computing System–Osaka*, pp. 17–19. The Computation Centre, Osaka Univ.

TORII, K. & IITAKA, Y. (1973). *Acta Cryst.* B**29**, 2799–2807.

WRIGHT, W. B. (1958). *Acta Cryst.* **11**, 632–642.