

Fig. 2. ORTEP view of a unit cell, *a* axis vertical, perpendicular to *b*.

bonds rather than about the C(10)—C(11) and C(10')—C(11') bonds] and twist angle 34° , was the only one of many tried which had a smaller calculated strain energy ($114.5 \text{ kJ mol}^{-1}$) than the X-ray structure ($115.3 \text{ kJ mol}^{-1}$); all others were at least 7.1 kJ mol^{-1} higher than the X-ray structure. The methylene proton chemical shifts calculated for this 'lowest-energy structure' are also shown in Table 2. They do not give a very good fit to the experimental values, but a roughly equimolar mixture with the MMPMI-minimized X-ray structure, which is what would be expected if these two conformations are the most stable but differ very little in energy, comes fairly close (Table 2); the discrepan-

cies may be due to lesser amounts of other less stable conformations.

Fig. 2 shows how the molecules pack in the crystal; apparently the conformation observed in the crystal gives better packing than the minimum-energy-solution conformation. The crystal consists of equimolar amounts of right- and left-handed molecules, stacked through the crystal in the *y* direction with the roughly flat aromatic rings above the methylene chains of the adjacent molecules in the stack; as can be seen in Fig. 1, the methylene chains in the molecules in the crystal, unlike those of the minimum-energy conformation, have a slightly concave arrangement which fits well with the slightly convex shape for the aromatic rings. The decrease in the angle of twist within the biphenyl system in the molecules in the crystal no doubt also occurs to provide better packing.

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Structure of the Thiopeptide (Z)-Glyt-Gly-OBzl

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Abstract. *N*-[(*N*-Benzyloxycarbonyl)thioglycyl]glycine benzyl ester, $\text{C}_{19}\text{H}_{20}\text{N}_2\text{O}_4\text{S}$, $M_r = 372.4$, monoclinic, $P2_1$, $a = 9.76$ (1), $b = 10.01$ (2), $c = 20.68$ (3) Å, $\beta = 69.7$ (1)°, $V = 1894.3$ Å³, $Z = 4$, $D_m = 1.30$, D_x

$= 1.30 \text{ Mg m}^{-3}$, $\lambda = 1.5418$ Å, $\mu(\text{Cu K}\alpha) = 1.69 \text{ mm}^{-1}$, $F(000) = 784$, $T = 293 \text{ K}$, $R = 0.048$ for 2958 reflections with $|F| \geq \sigma(F)$. The asymmetric unit contains two crystallographically independent peptide molecules in an extended form. The molecules are related to each other by a pseudo *a*-glide operation. They are arranged to form infinitely extended ribbons

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of antiparallel β -like sheets in the xy direction. The S atom, in the planar ($\omega = 177^\circ$) thiopeptide unit, is not involved in hydrogen bonding, the distance to the nearest noncovalently bonded atom being 3.01 Å. The lengths of the four different hydrogen bonds are in the range 2.85–2.90 Å.

Introduction. In a previous paper (la Cour, Hansen, Clausen & Lawesson, 1983), the molecular structure of the title compound was reported with regard to the influence of the thiopeptide unit on the geometry of the molecule. A more detailed account of the crystallographic work is given in this paper.

Experimental. The peptide was synthesized as described previously (Clausen, Thorsen & Lawesson, 1981). Colourless plates recrystallized from a hot solution of MeOH/Et₂O (1:4), crystal dimensions $1.0 \times 0.7 \times 0.07$ mm. D_m measured by gradient method in chlorobenzene-bromobenzene solution. Picker FC diffractometer with Ni filter. Cell constants by least-squares fit of 20 reflections with θ in the range 13–28°. Max. $2\theta = 120^\circ$, ω - 2θ scan, h -9 to 10, k -11 to 11, l 0 to 23, three standard reflections measured every 100 reflections showed no significant variations in intensity. Lp correction, but absorption ignored. A total of 6040 observations were reduced to a set of 2958 unique reflections, with $|F_o| \geq \sigma(F_o)$, used in the structure determination, $R_{int} = 0.0301$. The structure was solved by Patterson and difference Fourier methods (Fourier program *JIMDAP*, State University of New York at Buffalo), refined by full-matrix least squares on F , with anisotropic thermal parameters (Coppens & Hamilton, 1970). $w = 1/\sigma^2(F_o)$. Theoretical positions of H atoms were calculated with C-H 1.0, N-H 0.95 Å and included in the refinement with isotropic temperature factors. $R = 0.048$, $wR = 0.059$, $S = 1.79$. Largest $\Delta/\sigma = 0.30$ for non-H atoms. Max. and min. heights on final difference density map 0.46, -0.26 e Å⁻³. Atomic scattering factors: C, N and O from Cromer & Mann (1968), H from Stewart, Davidson & Simpson (1965), and S from *International Tables for X-ray Crystallography* (1968). Data-reduction programs used: *PROFILE*, *DATAPP* and *DSORTH* from State University of New York at Buffalo.

Discussion. Final parameters of the atoms are listed in Table 1.* The atomic numbering scheme is shown in Fig. 1 together with the principal torsion angles of the two crystallographically independent molecules *A* and *B*. As can be seen, they are related by a pseudo a -glide.

Table 1. *Atomic coordinates* ($\times 10^4$) *for non-H atoms and equivalent isotropic thermal parameters* (Å²) *with e.s.d.'s in parentheses*

$$B_{eq} = (8\pi^2/3) \sum_i \sum_j U_{ij} a_i^* a_j^* a_i a_j$$

	<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i> _{eq}
C(14A)	-4053 (7)	3551 (7)	3450 (3)	4.435 (3)
C(15A)	-3388 (7)	4303 (9)	3809 (3)	6.055 (4)
C(16A)	-4180 (11)	4711 (11)	4477 (4)	8.316 (6)
C(17A)	-5596 (13)	4388 (14)	4767 (4)	9.751 (8)
C(18A)	-6270 (8)	3680 (11)	4413 (4)	8.226 (6)
C(19A)	-5524 (7)	3250 (8)	3761 (3)	5.977 (4)
O(13A)	-3228 (7)	3077 (7)	2746 (3)	4.695 (4)
O(4A)	-3925 (4)	3580 (4)	2279 (2)	3.724 (2)
C(12A)	-3488 (5)	3053 (6)	1653 (2)	3.276 (3)
O(3A)	-2641 (4)	2146 (5)	1476 (2)	4.620 (2)
C(11A)	-4131 (5)	3784 (6)	1190 (2)	3.351 (3)
N(2A)	-4238 (5)	2952 (5)	641 (2)	3.204 (2)
C(10A)	-5165 (6)	1930 (5)	766 (3)	3.273 (3)
S(1A)	-6269 (1)	1500	1529 (1)	3.774 (1)
C(9A)	-5092 (6)	1090 (6)	143 (2)	3.485 (3)
N(1A)	-4564 (4)	1765 (5)	-514 (2)	3.348 (2)
C(8A)	-5471 (6)	2529 (5)	-715 (2)	2.904 (3)
O(2A)	-6623 (4)	2947 (4)	-323 (2)	3.981 (2)
O(1A)	-4955 (4)	2777 (4)	-1379 (2)	3.802 (2)
C(7A)	-5879 (5)	3530 (6)	-1666 (3)	3.739 (3)
C(1A)	-5262 (5)	3391 (6)	-2420 (3)	3.666 (3)
C(2A)	-5051 (6)	2135 (6)	-2731 (3)	4.570 (3)
C(3A)	-4499 (7)	2018 (7)	-3434 (3)	5.450 (4)
C(4A)	-4156 (7)	3125 (8)	-3843 (3)	5.892 (4)
C(5A)	-4344 (9)	4364 (8)	-3549 (3)	6.587 (5)
C(6A)	-4880 (8)	4510 (7)	-2838 (3)	5.454 (4)
C(14B)	738 (7)	3454 (7)	3411 (3)	4.187 (3)
C(15B)	529 (12)	2082 (8)	3420 (4)	8.866 (6)
C(16B)	-143 (14)	1452 (9)	4034 (4)	10.659 (8)
C(17B)	-634 (11)	2109 (11)	4636 (4)	8.280 (6)
C(18B)	-424 (9)	3465 (10)	4634 (3)	6.523 (5)
C(19B)	242 (7)	4098 (7)	4023 (3)	5.289 (4)
O(13B)	1503 (7)	4160 (7)	2748 (3)	4.919 (4)
O(4B)	904 (4)	3680 (4)	2246 (2)	3.683 (2)
C(12B)	1467 (5)	4207 (6)	1625 (3)	3.302 (3)
O(3B)	2350 (4)	5093 (4)	1474 (2)	4.122 (2)
C(11B)	891 (6)	3482 (6)	1139 (2)	3.299 (3)
N(2B)	837 (5)	4323 (5)	575 (2)	3.340 (2)
C(10B)	116 (5)	341 (5)	-688 (2)	3.054 (3)
S(1B)	1213 (1)	778 (2)	-1457 (1)	3.873 (1)
C(9B)	47 (7)	1143 (6)	-61 (3)	3.823 (3)
N(1B)	-450 (5)	449 (5)	580 (2)	3.625 (3)
C(8B)	-550 (6)	4648 (6)	-737 (3)	3.336 (3)
O(2B)	-1686 (4)	4250 (4)	-315 (2)	4.001 (2)
O(1B)	-67 (4)	4366 (4)	-1407 (2)	3.981 (2)
C(7B)	-1036 (6)	3533 (6)	-1635 (3)	3.985 (3)
C(1B)	-358 (6)	3326 (6)	-2386 (3)	3.878 (3)
C(2B)	1111 (6)	3201 (9)	-2718 (3)	5.746 (4)
C(3B)	1684 (7)	2915 (9)	-3406 (3)	6.381 (4)
C(4B)	801 (8)	2746 (9)	-3784 (3)	5.923 (4)
C(5B)	-653 (8)	2846 (9)	-3458 (3)	6.199 (5)
C(6B)	-1234 (6)	3142 (7)	-2772 (3)	5.076 (4)

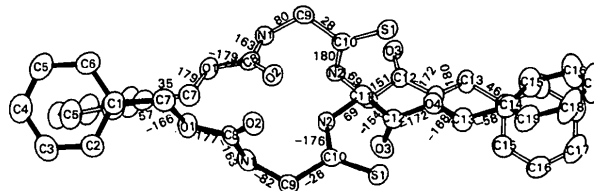


Fig. 1. Atomic numbering and torsion angles, shown on an *ORTEP* (Johnson, 1965) perspective drawing. [Nomenclature of the torsion angles is in agreement with the recommendations of IUPAC-IUB Commission on Biochemical Nomenclature (1970)]. Molecule *A* with dark bonds and *B* with light bonds. The thermal ellipsoids are drawn at 50% probability. Only non-H atoms are shown.

* Lists of structure factors, anisotropic thermal parameters and H-atom parameters have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 43426 (14 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 2. Comparison of bond lengths (Å) and angles (°) in the two molecules A and B

E.s.d.'s from ORFFE (Busing, Martin & Levy, 1964). Only non-H atoms are included. Bond lengths involving H atoms are in the range 0.7–1.2 Å.

	Molecule	
	A	B
C(1)–C(2)	1.394 (8)	1.363 (8)
C(2)–C(3)	1.370 (8)	1.366 (8)
C(3)–C(4)	1.364 (10)	1.360 (9)
C(4)–C(5)	1.365 (11)	1.347 (10)
C(5)–C(6)	1.386 (9)	1.365 (9)
C(6)–C(11)	1.385 (8)	1.369 (7)
C(11)–C(7)	1.471 (7)	1.476 (7)
C(7)–O(1)	1.451 (6)	1.456 (7)
O(1)–C(8)	1.312 (6)	1.331 (6)
C(8)–O(2)	1.210 (6)	1.217 (6)
C(8)–N(1)	1.340 (7)	1.367 (6)
N(1)–C(9)	1.444 (6)	1.425 (7)
C(9)–C(10)	1.519 (7)	1.507 (7)
C(10)–S	1.630 (5)	1.640 (5)
C(10)–N(2)	1.333 (7)	1.329 (6)
N(2)–C(11)	1.441 (6)	1.453 (6)
C(11)–C(12)	1.504 (6)	1.494 (7)
C(12)–O(3)	1.197 (6)	1.200 (6)
C(12)–O(4)	1.324 (6)	1.320 (6)
O(4)–C(13)	1.452 (6)	1.439 (7)
C(13)–C(14)	1.476 (8)	1.492 (8)
C(14)–C(15)	1.368 (9)	1.361 (9)
C(15)–C(16)	1.390 (9)	1.364 (11)
C(16)–C(17)	1.341 (11)	1.340 (12)
C(17)–C(18)	1.345 (15)	1.373 (12)
C(18)–C(19)	1.361 (11)	1.361 (9)
C(19)–C(14)	1.386 (9)	1.351 (8)
C(1)–C(2)–C(3)	120.5 (6)	121.5 (5)
C(2)–C(3)–C(4)	120.7 (6)	120.8 (6)
C(3)–C(4)–C(5)	119.7 (6)	118.0 (6)
C(4)–C(5)–C(6)	120.7 (7)	121.5 (6)
C(5)–C(6)–C(11)	119.9 (6)	121.1 (5)
C(6)–C(11)–C(7)	120.5 (6)	119.3 (5)
C(6)–C(11)–C(2)	118.5 (5)	117.0 (5)
C(2)–C(11)–C(7)	121.0 (5)	123.5 (5)
C(11)–C(7)–O(1)	107.5 (4)	108.5 (4)
C(7)–O(1)–C(8)	117.3 (4)	115.1 (4)
O(1)–C(8)–O(2)	124.4 (5)	125.7 (5)
O(1)–C(8)–N(1)	112.2 (4)	110.8 (5)
O(2)–C(8)–N(1)	123.4 (4)	123.8 (5)
C(8)–N(1)–C(9)	120.1 (4)	118.2 (6)
N(1)–C(9)–C(10)	115.9 (4)	116.1 (4)
C(9)–C(10)–S(1)	119.7 (4)	120.8 (4)
C(9)–C(10)–N(2)	115.6 (5)	116.1 (5)
S(1)–C(10)–N(2)	124.6 (4)	123.5 (6)
C(10)–N(2)–C(11)	121.4 (4)	121.7 (4)
N(2)–C(11)–C(12)	112.4 (5)	112.6 (4)
C(11)–C(12)–O(3)	124.8 (5)	125.8 (5)
C(11)–C(12)–O(4)	111.4 (4)	109.5 (4)
O(3)–C(12)–O(4)	123.8 (5)	124.6 (5)
C(12)–O(4)–C(13)	116.5 (4)	115.7 (4)
O(4)–C(13)–C(14)	108.9 (5)	107.8 (5)
C(13)–C(14)–C(15)	120.8 (6)	120.4 (6)
C(13)–C(14)–C(19)	120.7 (6)	122.5 (6)
C(19)–C(14)–C(15)	118.5 (6)	117.2 (6)
C(14)–C(15)–C(16)	119.8 (7)	119.4 (7)
C(15)–C(16)–C(17)	120.3 (8)	122.7 (8)
C(16)–C(17)–C(18)	120.4 (8)	118.5 (7)
C(17)–C(18)–C(19)	120.8 (7)	119.1 (7)
C(18)–C(19)–C(14)	120.2 (7)	123.2 (7)

Table 3. Hydrogen-bond lengths (Å) and angles (°)

E.s.d.'s less than 0.01 Å and less than 1°.

Donor	Acceptor	Symmetry	H–D	H...A	A...D	∠AHD
N(2A)	O(2B)	x, y, z	0.96	2.17	2.89	131.7
N(1A)	O(3B)	$-x, y - \frac{1}{2}, -z$	0.89	2.07	2.90	154.9
N(2B)	O(2A)	$x + 1, y, z$	1.02	2.05	2.88	136.9
N(1B)	O(3A)	$-x + 1, y + \frac{1}{2}, -z$	0.85	2.26	2.85	126.7

Apart from the sign of the conformational angles, the two molecules are similar, the only significant deviations are the angles determining the orientations of the phenyl groups. This phenomenon is often seen in crystals where phenyl groups are forced to pack together. They will do so by packing alternately edge on plane, caused by aromatic–aromatic interactions (Burlley & Petsko, 1985). The values of the torsion angles and the influence of the S atom on these have been discussed earlier (la Cour *et al.*, 1983). The bond distances and bond angles of the two molecules are compared in Table 2. As to the backbones, there are no significant differences between them, and no unusual values are found. There are some differences in the bond lengths within the phenyl groups, but they can be explained by the high thermal motions of these groups. Four different intermolecular H bonds are found in the cell; their geometries are shown in Table 3. The hydrogen-bond system resembles that found in several oligopeptides; it forms infinitely extended antiparallel β -sheets in the crystals (Yamane, Shiraishi & Ashida, 1985), although the torsion angles differ from the values characterizing the ideal β -sheets (ϕ, ψ) = (–120, 120°). Most obvious is the deviation of the angle defined by N(1)–C(9)–C(10)–N(2), ψ = –26 (28°). This conformation of the molecules seems to be optimal for the N atoms of both amide groups to act as donors in hydrogen bonding, while avoiding steric hindrance from the bulky S atom. The bond lengths of the hydrogen bonds are in a narrow range (2.85–2.90 Å), which corresponds to the mean value of the hydrogen-bond lengths in peptides and proteins. A comparison with

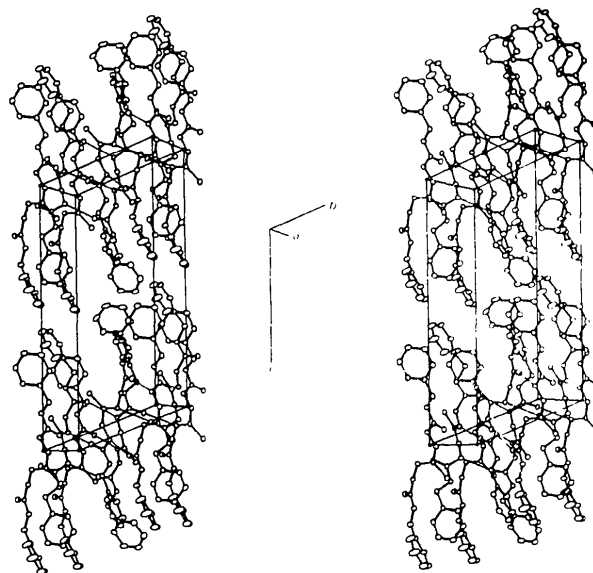


Fig. 2. Stereoscopic diagram of the crystal structure.

thiopeptide groups in two thiopeptide containing tripeptides (Jensen, Lawesson, Bardi, Piazzesi & Toniolo, 1985) shows a significantly longer C—S bond length, 1.663 Å, as compared with 1.635 Å in this study and a correspondingly shorter amide bond length. This indicates a redistribution of electrons in the peptide unit, probably caused by the delocalization of electrons on the S atom since this atom acts as acceptor in a weak hydrogen-bond system.

The influence of the hydrogen bonds on the packing of the molecules in the unit cell is shown in Fig. 2. Molecules *A* and *B* are alternately arranged to form ribbons extended along *a* and *b* axes; obviously the β -like sheets give the crystals a stability in these directions. Along the *c* axis, the ribbons are separated by regions that are very rich in phenyl groups. Together these features explain the macroscopic appearance of the crystals as thin plates, with the *c* axis perpendicular to the plates.

Both in the oxopeptide and the thiopeptide units, there are only minor deviations from the planar *trans* form ($\omega = 180^\circ$), the angles being $\omega_1 = -176$ (180°) and $\omega_2 = -172$ (172°). The S atom is not involved in any hydrogen bonding, the distance to the nearest non-covalently bonded atom, which is an H atom, is 3.01 Å, in agreement with the sum of the van der Waals radii of the atoms involved.

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Structure of the Dithiopeptide (Z)-Glyt-Glyt-Gly-OBzl

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Abstract. *N*-(Benzyloxycarbonyl)thioglycylthioglycylglycine benzyl ester, $C_{21}H_{23}N_3O_4S_2$, $M_r = 445.6$, triclinic, $P\bar{1}$, $a = 10.291$ (4), $b = 14.880$ (6), $c = 8.033$ (3) Å, $\alpha = 97.72$ (3), $\beta = 110.13$ (3), $\gamma = 73.46$ (3)°, $V = 1106.3$ (9) Å³, $Z = 2$, $D_m = 1.30$, $D_x = 1.34$ Mg m⁻³, $\lambda(\text{Cu } K\alpha) = 1.5418$ Å, $\mu = 2.41$ mm⁻¹, $F(000) = 468$, $T = 293$ K, $R = 0.044$ for 1479 unique reflections with $F_o > \sigma(F_o)$. The peptide molecules are in a bent form, owing to the unusual torsion angle $\psi_1 = -8^\circ$ at the first α -C atom and contain an extremely short thiopeptide bond, 1.301 Å. The packing of the molecules follows a well known scheme with ribbons of hydrogen bonds alternating

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with regions rich in phenyl groups. The S atoms are not involved in hydrogen bonding; the distance to the nearest amide H atom is more than 3.5 Å.

Introduction. The structural study of (Z)-Glyt-Glyt-Gly-OBzl is part of an investigation of the influence of thiopeptide units on the conformation and hydrogen-bonding pattern in a range of endothiopeptides synthesized and described by Clausen (1982). These types of compounds are of interest in the search for new drugs of potential use in neuropharmacology.

Experimental. The compound was synthesized as reported previously, m.p. 389–391 K (Clausen, 1982). Crystals shaped as parallelepipeds were obtained from an MeOH/H₂O vapour diffusion system. D_m measured

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