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Structures of L-Phenylalanine Dimers, *N*-(*tert*-Butoxycarbonyl)-L-phenylalanyl-L-phenylalanine Benzyl Ester (Boc-Phe-Phe-OBzl) and L-Phenylalanyl-L-phenylalanine Ethyl Ester Trifluoroacetate (Phe-Phe-OEt.Tfa)

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Abstract

The crystal structures of the title compounds have been determined by the direct method and refined by the block-diagonal least-squares method. Boc-Phe-Phe-OBzl has space group $P2_1$, with $a = 14.363$ (3), $b = 19.016$ (5), $c = 5.077$ (1) Å, $\beta = 97.02$ (2)°, $V = 1376.3$ (8) Å³, $Z = 2$, and $R = 0.070$ for 1921 reflections; Phe-Phe-OEt.Tfa has space group $P2_12_12_1$, with $a = 16.507$ (4), $b = 24.927$ (7), $c = 5.650$ (1) Å, $V = 2325$ (1) Å³, $Z = 4$, and $R = 0.074$ for 1544 reflections. The former crystallizes in the parallel β pleated sheet. Deviation of the main-chain conformation from that of the typical β sheet due to the substitution of bulky terminal groups is observed. The latter molecule is not in the β sheet, but has a column structure with a hydrophilic core of hydrogen bonds and a hydrophobic shell.

Introduction

Difficulties in the crystallization of peptides often restrict X-ray conformational studies in the solid state. When the peptide to be studied has large hydrophobic side chains, it becomes more difficult to obtain crystals large enough for X-ray analysis. Crystal structure studies of peptides involving two successive phenyl-

alanine residues so far reported are limited to dipeptides and tripeptides. These crystal structures can be classified into either of the following two groups on the basis of intermolecular interactions: (1) parallel β pleated-sheet-type structures stabilized by a pair of intermolecular hydrogen bonds, and (2) salt type in which the crystal packing is determined by hydrogen bonds and electrostatic interactions between peptides and counter-ions. In both cases, however, clusters of the phenylalanine side chains are observed in the crystal structures.

We have been studying the solid-state structures of poly(α -amino acids), which carry large hydrophobic side chains, by X-ray diffraction and have found the coexistence of ω - and α -helices in poly(L-phenylalanine) on the basis of X-ray fiber photographs (Yamashita, Yamane, Ashida, Yamashita & Yamashita, 1979). In this case, the side-chain–side-chain interactions must play an important role in determining the type of helix. To reveal the role of phenyl groups in peptide conformations, some phenylalanine oligomers have been synthesized and their crystal structures studied. This report deals with the crystal structures of *N*-(*tert*-butoxycarbonyl)-L-phenylalanyl-L-phenylalanine benzyl ester (Boc-Phe¹-Phe²-OBzl) and L-phenylalanyl-L-phenylalanine ethyl ester trifluoroacetate (Phe¹-Phe²-OEt.Tfa), both of which have two phenylalanyl residues. The former belongs to the type (1) mentioned above, and the latter to (2).

Experimental

Crystal specimens

Boc-Phe-Phe-OBzl was prepared by the DCC (*N,N'*-dicyclohexylcarbodiimide) coupling of the Boc-Phe.DCHA [dicyclohexylammonium *N*-(*tert*-butoxycarbonyl)-L-phenylalaninate] and Phe-OBzl.TosOH (L-phenylalanine benzyl ester *p*-toluenesulfonate). Phe-Phe-OEt.Tfa was prepared by the DCC coupling of Boc-Phe.DCHA and Phe-OEt.HCl (L-phenylalanine ethyl ester hydrochloride), followed by the elimination of the Boc group by solvolysis with trifluoroacetic acid.

Boc-Phe-Phe-OBzl was crystallized from an ethyl acetate-*n*-hexane solution and Phe-Phe-OEt.Tfa from an aqueous acetone solution. Both crystals are needles elongated in the *c* direction.

X-ray measurements

The lattice constants and intensity data were derived from measurements on a Rigaku four-circle diffractometer using graphite-monochromatized Cu *K* α radiation. Intensities were measured by the ω - 2θ scanning method. Backgrounds were counted at both ends of the diffraction peak. The details of the measurement and results are summarized in Table 1. Intensities were corrected for Lorentz and polarization effects, but not for absorption.

Structure determination

The structures were solved by the multi-solution tangent-formula program *MULTAN* 78 (Main, Hull, Lessinger, Germain, Declercq & Woolfson, 1978). The parameters were refined by the block-diagonal least-squares program *HBLS* V (Ashida, 1973). The function minimized was $\sum w(|F_o| - |F_c|)^2$ with $w = [\sigma^2(F_o) + a|F_o| + b|F_o|^2]^{-1}$, where $\sigma(F_o)$ is the standard deviation based on the counting statistics. Difference Fourier syntheses yielded the positions of the H atoms, which were located at stereochemically

Table 1. *Additional crystallographic and experimental data*

	Boc-Phe-Phe-OBzl	Phe-Phe-OEt.Tfa
Chemical formula	C ₃₀ H ₃₄ N ₂ O ₅	C ₃₀ H ₃₄ N ₂ O ₅ ·C ₂ F ₃ O ₂ ⁻
Formula weight	502.62	454.46
<i>d</i> _c (Mg m ⁻³)	1.213	1.301
<i>d</i> _a (Mg m ⁻³)	1.206	1.283
Crystal size (mm)	0.20 × 0.13 × 0.13	0.4 × 0.1 × 0.1
<i>F</i> (000)	556	952
μ (Cu <i>K</i> α) (cm ⁻¹)	6.765	10.023
Scan technique	ω - 2θ	ω - 2θ
Scan range ($2\theta_{\max}$) (°)	138	125
Scan width (°)	1.0 + 0.15 tan θ	1.5 + 0.15 tan θ
Scan speed (° min ⁻¹)	13	7 (0° < 2θ ≤ 90°) 2 (90° < 2θ ≤ 125°)
Background counting time (s)	0.75	3 (0° < 2θ ≤ 90°) 10 (90° < 2θ ≤ 125°)
Number of reflections	2566 [1921 with <i>F</i> ≥ 3 σ (<i>F</i>)]	2157 [1544 with <i>F</i> ≥ 3 σ (<i>F</i>)]

reasonable positions and assigned isotropic thermal parameters equal to those of the carrier atoms.

(a) Boc-Phe-Phe-OBzl

The best set of phases with the highest combined figure of merit gave an interpretable structure of 22 atoms out of 37 nonhydrogen atoms. Successive Fourier calculations revealed the remaining atomic positions. The final refinement gave *R* = 0.070 for 1921 reflections which had $|F_o| > 3\sigma(F_o)$. The values *a* and *b* were -0.247 and 0.009, respectively. Table 2 contains the final positional and thermal parameters.*

* Lists of anisotropic thermal parameters, the hydrogen positional parameters and structure factors have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 36911 (29 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 2. Boc-Phe-Phe-OBzl: *atomic positional* ($\times 10^4$) *and thermal parameters, with standard deviations in parentheses.*

*B*_{eq} is the equivalent isotropic temperature factor, calculated from the anisotropic temperature coefficients (Hamilton, 1959).

	<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i> _{eq} (Å ²)
C(1)	938 (4)	4970 (3)	2370 (10)	6.0 (2)
C(2)	62 (5)	5589 (2)	-1510 (11)	7.2 (3)
C(3)	-828 (4)	4929 (3)	1610 (10)	6.0 (2)
C(4)	72 (3)	4961 (3)	290 (8)	4.9 (2)
O(01)	134 (2)	4367 (1)	-1506 (5)	4.6 (1)
C(00)	141 (2)	3711 (2)	-656 (6)	3.1 (2)
O(02)	47 (2)	3542 (1)	1613 (5)	4.6 (1)
N(1)	245 (2)	3253 (2)	-2617 (5)	3.2 (1)
C(A1)	116 (2)	2515 (0)	-2333 (6)	3.1 (1)
C(B1)	-791 (3)	2258 (2)	-3985 (8)	4.0 (2)
C(P11)	-1644 (3)	2598 (2)	-3096 (8)	4.4 (2)
C(P12)	-1971 (3)	3220 (2)	-4201 (10)	5.5 (2)
C(P13)	-2762 (4)	3551 (2)	-3411 (13)	7.3 (3)
C(P14)	-3232 (3)	3213 (3)	-1454 (11)	6.9 (3)
C(P15)	-2910 (4)	2615 (3)	-331 (11)	7.2 (3)
C(P16)	-2123 (3)	2291 (2)	-1550 (9)	5.2 (2)
C(O1)	949 (3)	2150 (2)	-3264 (7)	3.4 (1)
O(1)	1042 (2)	2083 (2)	-5640 (5)	4.8 (1)
N(2)	1620 (2)	1905 (1)	-1378 (6)	3.4 (1)
C(A2)	2486 (3)	1611 (2)	-2167 (7)	3.8 (2)
C(B2)	3178 (3)	2196 (2)	-2735 (8)	4.4 (2)
C(P21)	3539 (3)	2655 (2)	-502 (8)	4.6 (2)
C(P22)	2999 (3)	3219 (2)	349 (10)	5.9 (2)
C(P23)	3326 (4)	3625 (3)	2432 (12)	6.9 (3)
C(P24)	4225 (4)	3517 (3)	3748 (11)	7.6 (3)
C(P25)	4755 (4)	2975 (4)	2898 (11)	7.7 (3)
C(P26)	4417 (3)	2557 (2)	882 (11)	6.1 (2)
C(O2)	2897 (3)	1117 (2)	-11 (8)	4.1 (2)
O(2)	2639 (3)	1016 (1)	2039 (6)	6.2 (2)
O(03)	3616 (2)	752 (2)	-941 (7)	7.1 (2)
C(BZ1)	4036 (4)	209 (3)	779 (13)	7.8 (3)
C(BZ2)	5021 (3)	430 (3)	1971 (11)	6.0 (2)
C(BZ3)	5757 (4)	149 (4)	1056 (13)	9.8 (4)
C(BZ4)	6671 (5)	362 (4)	2201 (23)	11.8 (5)
C(BZ5)	6786 (5)	874 (4)	4035 (16)	10.8 (4)
C(BZ6)	5998 (6)	1090 (4)	5030 (18)	13.7 (5)
C(BZ7)	5153 (5)	887 (6)	3924 (15)	12.8 (6)

Table 3. *Hydrogen bonds in Boc-Phe-Phe-OBzl*

Donor (D)	Hydrogen (H)	Acceptor (A)	Distance (Å)			Angle (°)
			D...A	D—H	H...A	D—H...A
N(1)	H(N1)	O(02 ⁱ)	2.960 (5)	0.84 (4)	2.16 (4)	159 (4)
N(2)	H(N2)	O(1 ⁱⁱ)	3.143 (5)	1.08 (4)	2.07 (4)	170 (3)
C(42)	H(42)	O(2 ⁱ)	3.184 (6)	0.97 (5)	2.38 (5)	140 (4)

Symmetry codes: (i) $x, y, -1.0 + z$; (ii) $x, y, 1.0 + z$.Table 4. *Phe-Phe-OEt.Tfa: atomic positional ($\times 10^4$) and thermal parameters, with standard deviations in parentheses* B_{eq} is the equivalent isotropic temperature factor, calculated from the anisotropic temperature coefficients (Hamilton, 1959).

	<i>x</i>	<i>y</i>	<i>z</i>	B_{eq} (Å ²)
N(1)	2473 (3)	4526 (2)	11927 (12)	4.9 (2)
C(A1)	2964 (4)	4036 (2)	11327 (12)	4.0 (2)
C(B1)	2368 (4)	3584 (2)	10830 (16)	5.0 (3)
C(11)	2773 (4)	3062 (3)	10191 (13)	4.9 (3)
C(12)	2563 (7)	2807 (3)	8192 (17)	7.6 (5)
C(13)	2879 (10)	2317 (4)	7621 (22)	11.1 (8)
C(14)	3441 (8)	2066 (4)	9132 (21)	8.7 (6)
C(15)	3643 (6)	2311 (3)	11112 (25)	8.4 (5)
C(16)	3323 (5)	2817 (3)	11593 (18)	6.8 (4)
C(O1)	3479 (3)	4171 (2)	9225 (12)	3.7 (2)
O(1)	3186 (3)	4366 (2)	7422 (9)	5.6 (2)
N(2)	4269 (3)	4058 (2)	9510 (10)	4.4 (2)
C(A2)	4854 (3)	4148 (2)	7603 (12)	4.1 (2)
C(B2)	5677 (4)	4299 (3)	8780 (13)	5.0 (3)
C(21)	6370 (3)	4298 (2)	7042 (12)	4.3 (3)
C(22)	6385 (4)	4629 (3)	5138 (14)	5.1 (3)
C(23)	7045 (4)	4619 (3)	3551 (14)	5.9 (4)
C(24)	7692 (4)	4284 (3)	3989 (16)	5.8 (3)
C(25)	7686 (4)	3969 (3)	5937 (19)	6.2 (4)
C(26)	7026 (4)	3962 (3)	7436 (15)	5.1 (3)
C(O2)	4950 (4)	3644 (3)	6126 (13)	4.5 (3)
O(2)	4797 (3)	3612 (3)	4042 (10)	6.0 (2)
O(3)	5217 (3)	3227 (2)	7361 (10)	5.8 (2)
C(E1)	5348 (7)	2737 (3)	6149 (21)	8.1 (5)
C(E2)	5826 (10)	2399 (5)	7414 (45)	15.4 (12)
C(F1)	266 (4)	4121 (3)	7615 (20)	6.9 (4)
C(F2)	1025 (3)	4402 (3)	6865 (15)	4.8 (3)
O(4)	1320 (4)	4199 (3)	5066 (13)	9.4 (4)
O(5)	1282 (3)	4749 (2)	8131 (14)	6.8 (3)
F(1)	−347 (3)	4301 (4)	6599 (22)	16.6 (7)
F(2)	274 (6)	3622 (3)	7343 (30)	19.8 (9)
F(3)	73 (5)	4170 (4)	9792 (18)	17.0 (7)

(b) *Phe-Phe-OEt.Tfa*

The best phase set with the highest combined figure of merit gave all the nonhydrogen-atom positions. The final refinement gave $R = 0.074$ for 1544 reflections which had $|F_o| > 3\sigma(F_o)$. The values a and b were 0.032 and 0.003, respectively. Table 4 contains the final positional and thermal parameters.*

* See deposition footnote.

The atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1974). All the calculations were carried out on the FACOM M-200 computer of Nagoya University Computation Center.

Results and discussion

(a) *Boc-Phe-Phe-OBzl*

Bond lengths, bond angles and torsion angles are shown in Fig. 1(a,b,c), together with the serial numbering of atoms in the molecule. Bond lengths and angles are in accordance with the mean values observed in other peptides (Marsh & Donohue, 1967) within the experimental errors. The definition of the torsion angles given by the IUPAC–IUB Commission on Biochemical Nomenclature (1970) is adopted. The molecule, drawn by *ORTEP* II (Johnson, 1976), is shown in Fig. 2. The crystal structure is shown in Fig. 3 and hydrogen bonds are listed in Table 3.

As is shown in Fig. 1(c), the main chain of this peptide takes an extended conformation, which is classified as a parallel β pleated sheet according to the torsion angles and mode of hydrogen bonding. The torsion angles (ϕ, ψ) of Phe¹ [-131.4 (4), 102.3 (4) $^\circ$] are not very close to those of the parallel β -pleated-sheet structure, $\phi = -119^\circ$ and $\psi = 113^\circ$ (Schellman & Schellman, 1964), but the present peptide possesses all the main features of the parallel sheet. Fig. 4 shows that the molecules separated by the c -axis translation are connected by the two N—H...O hydrogen bonds to form an infinite sheet with a single pleat. The N...O distances of 2.960 and 3.143 Å are somewhat longer than those of 2.90 Å given by Marsh & Donohue (1967). The distance between adjacent chains within the sheet is the c -axis period, 5.077 Å.

The pleat angle, or dihedral angle between the two peptide planes, is 116.0 (1) $^\circ$. The O(01)—C(A2) distance, corresponding to the pleat distance along chains in the β pleated sheet, is 6.266 (4) Å. The lengths of the peptide units are 3.546 (4) Å [O(01)—C(A1)] and 3.805 (5) Å [C(A1)—C(A2)]. The main chain of the present peptide bends at the C(A1) atom as a hinge, so that the sheet is pleated.

might be caused by the steric effects due to the substitution of a bulky Boc group.

The hydrogen-bond length $N\cdots O$ of the C-terminal side is elongated to 3.143 (5) Å from the normal value 2.90 Å. This seems to be an effect of the contact between the C(42) and O(2) atoms, 3.184 (6) Å (Table 3). This contact may be considered as a $C-H\cdots O=C$ hydrogen bond. An example of the C^α atom of a peptide playing the role of hydrogen-bond donor was reported by Marsh, Ramakumar & Venkatesan (1976) in the structure of Gly-D,L-Phe.

The parallel β -pleated-sheet structures in oligopeptides were reported in eight crystals, many of which contain phenylalanine residues. The crystal of a phenylalanine dimer Cl-Ac-Phe-Phe-OEt [Cl-Ac: *N*-(chloroacetyl) (Wei, Doherty & Einstein, 1972)] also shows the parallel β -pleated-sheet structure, but small but significant differences are found between the torsion angles of the main chains. Furthermore, the side-chain conformations are different; χ_1^1 and χ_2^1 are -61.9 (4) and 63.3 (5)° for the present dimer and -175 and -71 ° for Cl-Ac-Phe-Phe-OEt. Such differences can be attributed to the substitution of the terminal groups with bulky *tert*-butyl and benzyl groups. Thus, the stacking of the additional bulky groups leads to the alteration of the side-chain conformation and critically affects that of the main chain in the present peptide.

The hydrogen-bonding moiety is encompassed by the side groups and thus, as a whole, a hydrophobic sheet running along the *c* axis is formed. A crystal of this peptide is considered to be an assembly of these sheets with van der Waals forces between the hydrophobic groups, which consequently show large thermal vibrations. The interchain distance in the sheet (*i.e.* the *c*-axis period, 5.077 Å) is somewhat longer than the average value in the peptides with parallel β -sheet structures (4.95 Å), because of the presence of the bulky *tert*-butyl group.

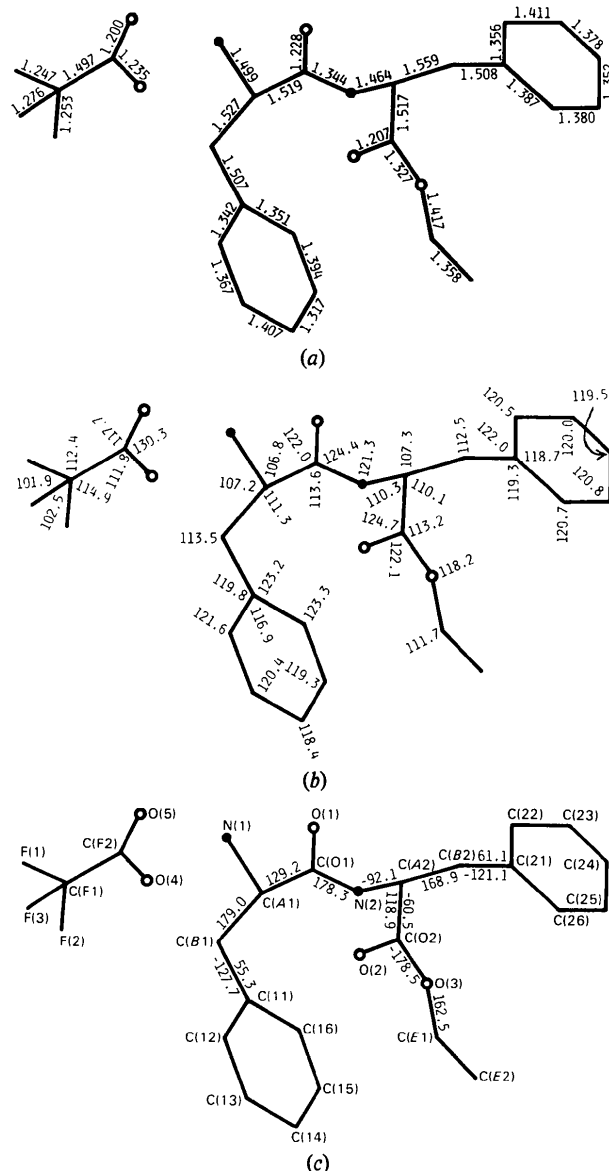


Fig. 5. Phe-Phe-OEt.Tfa: (a) bond lengths (Å). Estimated standard deviations are 0.008–0.028 Å. (b) Bond angles (°). [C(F2)–C(F1)–F(3) 115.9, F(1)–C(F1)–F(2) 108.0°.] Estimated standard deviations are 0.5–1.4°. (c) Torsion angles (°). Estimated standard deviations are 0.5–1.3°.

(b) Phe-Phe-OEt.Tfa

Bond lengths, bond angles and torsion angles are given in Fig. 5. A drawing of the molecule is shown in Fig. 6. The crystal structure is shown in Fig. 7 and the hydrogen bonds are listed in Table 5.

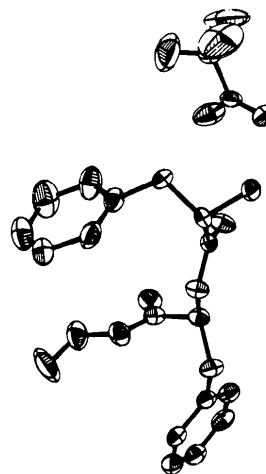


Fig. 6. ORTEP drawing of Phe-Phe-OEt.Tfa. Thermal ellipsoids are drawn at the 30% probability level.

The crystal structure is stabilized by a three-dimensional network of hydrogen bonds. There are four protons on a molecule which can participate in hydrogen bonding and all are involved in intermolecular hydrogen bonds. There are five neighbors to the protonated nitrogen atom N(1): O(5ⁱⁱⁱ), O(5ⁱ), O(4ⁱⁱ), O(1ⁱⁱⁱ), and O(1ⁱ) at distances of 2.820 (10), 2.962 (10), 2.726 (10), 2.982 (8), and 2.832 (8) Å, respectively. By considering the disposition of the atoms, it was concluded that N(1)···O(1ⁱ) and N(1)···O(1ⁱⁱⁱ) are normal ionic contacts because the N—H···O angles are 107 (7) and 102 (6)°, respectively, which are not compatible with the hydrogen-bonding geometry. The hydrogen-bonding scheme is shown in Fig. 8.

The conformation of this peptide molecule resembles that of Thr-Phe-OBzl(NO₂).HBr [L-threonyl-L-phenylalanine *p*-nitrobenzyl ester hydrobromide (Mallikarjunan, Rao & Venkatesan, 1969)]. The hydrogen-bonding scheme, except one of the hydroxyl groups of the threonyl residue, is the same as that of the present peptide; the hydrogen-bonding network around the terminal ammonium group and the peptide N atom make a hydrophilic core extending along a twofold screw axis parallel to the *c* axis. The torsion angles of the side chains are also very similar. The crystal packing is, however, very different, owing to the presence of an additional hydrogen bond

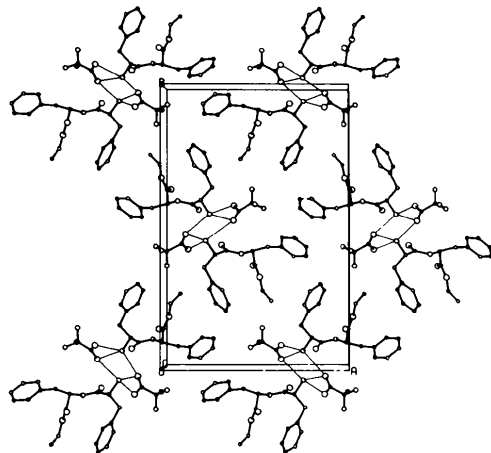


Fig. 7. Crystal structure of Phe-Phe-OEt.Tfa along the *c* axis.

involving the threonyl hydroxyl group in Thr-Phe-OBzl(NO₂).HBr. In the present peptide crystal, the hydrophilic core is surrounded by a hydrophobic shell which consists of ethyl, trifluoromethyl and benzyl groups and thus, as a whole, a column structure running along the *c* axis is formed. The columns are assembled in the crystal with only van der Waals forces between the hydrophobic side chains. Thus the side chains suffer from large thermal vibrations.

In the trifluoroacetate ion, the three F atoms have extraordinarily large temperature factors of $B_{eq} = 17\text{--}20 \text{ Å}^2$, which is also observed in NH₄.Tfa (Cruickshank, Jones & Walker, 1964). It seems that they undergo a hindered rotation about the C(F1)—C(F2) bond.

Hydrogen bonding plays an important role in forming the β -sheet and column structure, as is shown in the present phenylalanine dimers. Its directional property forces the peptide molecules to form only one- or two-dimensional arrays. As these arrays are assembled into crystals only with van der Waals forces, crystallization of these peptides depends upon whether the compact accommodation of the large hydrophobic side groups is accomplished or not. The present phenylalanine dimers may offer successful examples of the accommodation of phenyl rings in the crystal lattice. Many phenylalanine oligomers larger than trimers, as far as we know from their syntheses, occur usually as an amorphous powder, and it is not easy to obtain good crystals for X-ray analysis. It is worth mentioning that too many large hydrophobic side chains prevent the

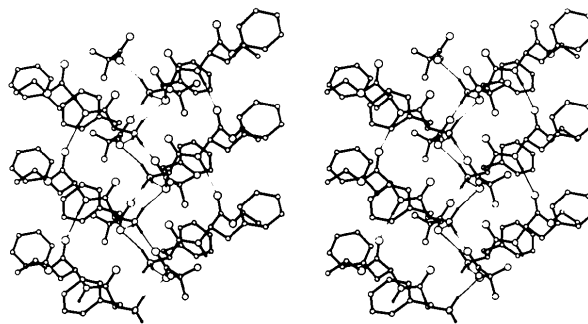


Fig. 8. Hydrogen-bonding scheme of Phe-Phe-OEt.Tfa. Hydrogen bonds are drawn with thin lines. The *c* axis points upward.

Table 5. *Hydrogen bonds in Phe-Phe-OEt.Tfa*

Donor (<i>D</i>)	Hydrogen (<i>H</i>)	Acceptor (<i>A</i>)	Distance (Å)			Angle (°)
			<i>D</i> ··· <i>A</i>	<i>D</i> — <i>H</i>	<i>H</i> ··· <i>A</i>	<i>D</i> — <i>H</i> ··· <i>A</i>
N(1)	H(N11)	O(5 ⁱⁱⁱ)	2.820 (10)	0.86 (9)	2.00 (9)	161 (9)
N(1)	H(N12)	O(5 ⁱ)	2.962 (10)	0.95 (9)	2.07 (9)	156 (8)
N(1)	H(N13)	O(4 ⁱⁱ)	2.726 (10)	0.93 (9)	1.80 (9)	175 (8)
N(2)	H(N2)	O(2 ⁱⁱ)	2.924 (8)	0.99 (9)	1.94 (9)	173 (8)

Symmetry codes: (i) *x*, *y*, *z*; (ii) *x*, *y*, 1.0 + *z*; (iii) 0.5 − *x*, 1.0 − *y*, 0.5 + *z*.

growth of fairly ordered crystal lattices for such phenylalanine oligomers.

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La Structure du *N,N'*-Heptaméthylène-dibenzamide

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Abstract

Crystals of *N,N'*-heptamethylenedibenzamide, $C_{21}H_{26}N_2O_2$, are monoclinic and belong to space group $P2_1/n$. The unit-cell dimensions are $a = 5.087$ (3), $b = 44.172$ (14), $c = 8.496$ (5) Å and $\beta = 91.08$ (5)°, $V = 1908.7$ Å³, $F(000) = 728$, $M_r = 338.44$, $Z = 4$, $d_o = 1.14$, $d_c = 1.177$ Mg m⁻³. The structure was solved by direct methods using 1501 independent reflections whose intensities were measured on a Nonius CAD-4 diffractometer. Block-diagonal least-squares refinement of the coordinates and thermal parameters was concluded when $R_w = 0.054$. The molecule consists of a central nearly planar $NH-(CH_2)_7-NH$ sequence between two benzamide groups. The dihedral angles between the methylenic sequence and the benzene rings are 117.2 (18) and 124.5 (4)° respectively. The distance between the centers of the benzene rings is 16.789 (8) Å. Each molecule is connected through four hydrogen bonds to two others, forming ribbons parallel to the *ab* plane and extending in the *a* direction. This hydrogen bonding is characterized by the following parameters: $N(1)-H(N1) = 0.91$ (3), $H(N1) \cdots O(1') = 2.07$ (3) Å, $N(1)-H(N1) \cdots O(1') = 151$ (3)° and $N(2)-H(N2) = 0.91$ (3), $H(N2) \cdots O(2') = 2.03$ (3) Å, $N(2)-H(N2) \cdots O(2') = 153$ (3)°.

Introduction

Une étude systématique des composés de la série *N,N'*-oligométhylène-dibenzamide a été entreprise dans le but d'étendre les informations géométriques et conformationnelles déduites de ces composés modèles aux polymères parents, les poly(oligométhylènes-téréphthalamides). Dans un travail antérieur (Brisse, Marchessault & Pérez, 1979) il avait été établi qu'il existait une relation structurale entre le composé modèle et son polyester apparenté, tant du point de vue de la géométrie que de la conformation. La présente étude a pour but de s'assurer qu'une telle similitude existe aussi lorsque des ponts hydrogènes sont présents et lorsque le nombre de groupes méthylènes dans la région aliphatique de la molécule est impair.

Partie expérimentale

Le *N,N'*-heptaméthylène-dibenzamide a été synthétisé par addition lente de chlorure de benzoyle à une solution d'heptanediamine-1,7 dans l'oxyde d'éthyle. Le tout se faisait en présence de pyridine comme capteur de protons et sous atmosphère d'azote. Le précipité ainsi obtenu fut neutralisé par une solution