Structure of some peptides isolated from the soluble fraction of the tryptic digest of S-sulpho-trypsinogen

The following peptides isolated from the soluble fraction of the tryptic digest of S-sulpho-trypsinogen¹ are identical with peptides isolated from the tryptic digest of diisopropylphosphoryl-trypsin²

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T-2: Glu(NH_2)-Thr-Ala-Ileu-Ser-Asp(NH_2)

T-45: Gly-Asp(NH_2)-Thr-Lys

T-47: Ser-Ser-Gly-Thr-Ser-Tyr-Pro-Asp-Val-Leu-Lys

T-52: Ser-Ala-Ala-Ser-Leu-Asp(NH_2)-Ser-Arg

T-55: Leu-Lys

T-56: Ser-Gly-Ileu-Glu(NH_2)-Val-Arg

T-59: Ser-Arg

T-64: Leu-Lys-Ser-Ala-Ala-Ser-Leu-Asp(NH_2)-Ser-Arg
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The structures of some other peptides isolated from the soluble fraction of the tryptic digest of S-sulpho-trypsinogen¹, namely those peptides remaining in solution after acidifying the tryptic digest to pH 3.0, are shown in Table I.

TABLE I STRUCTURES OF THE ISOLATED PEPTIDES

Designation of the peptide	Structure
T-23	Ser-Ser-Cys-Lys
T-24	Val-Ala-Ser-(Leu, Ser, Pro, Ileu, Thr, Ser, Cys, Ala, Gly, Ala, Ser, Thr, Glu, Cys) - Leu-Ileu-Ser-Gly-Try-Gly-Asp(NH ₂)-Thr-Lys
T-26	Ala-Pro-lleu-Leu-Ser-Asp-Ser-Ser-Cys-Lys
T-27	Ser-Ala-Tyr-Pro-Gly-Glu(NH2)-Ileu-Thr-Ser-Asp(NH2)
T-30	Cys-Leu-Lys-Ala-Pro-Ileu-Leu-Scr-Asp-Ser-Ser-Cys-Lys
T-37	Val-Asp-Asp-Asp-Asp-Lys-Ileu-Val-Gly-Gly-Tyr-Thr-(Asp, Cys, Thr Pro. Gly. Ala, Val)-Tyr
T-53	Ser-Ala-Tyr-Pro-Gly-Glu(NH ₂)-Ileu-Thr-Ser-Asp(NH ₂)-Met-Phe-Cys-Ala-Gly-Tyr-Leu-Glu-Gly-Gly-Lys
T-61	Asp(NH ₂)-Lys-Pro-Gly-Val-Tyr-Thr-Lys
T-62	Lys-Pro-Gly-Val-Tyr-Thr-Lys

The structures were established on the basis of cleavage with chymotrypsin (EC 4.5.5.5), pepsin (EC 3.4.4.10), subtilopeptidase A (EC 3.4.4.16), leucine aminopeptidase (EC 3.4.4.1), separation and characterization of fragments by chromatography on ion-exchange resins and on paper and by high-voltage paper electrophoresis. The N- and C-terminal groups were determined by dinitrophenylation and hydrazinolysis. The quantitative amino acid composition was determined by an amino acid analyzer³.

In addition to the above peptides the following three peptides were obtained from the tryptic digest of S-sulpho-trypsinogen, viz.

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    T-1: Asp(NH<sub>2</sub>) - (Ser<sub>3</sub>, Cys<sub>2</sub>, Glu(NH<sub>2</sub>), Gly<sub>4</sub>, Asp, Pro, Val<sub>2</sub>) - Lys
    T-29: Ser - (Ala, Tyr, Pro) - Gly - Glu(NH<sub>2</sub>) - lieu - Thr - Ser - Asp(NH<sub>2</sub>) - Met - Phe - (Cys, Ala, Gly, Tyr, Leu, Glu, Gly, Gly, Lys, Asp(NH<sub>2</sub>), Ser, Cys, Glu(NH<sub>2</sub>), Gly, Gly, Asp, Ser, Gly, Pro, Val, Val, Cys, Ser, Gly) - Lys
    T-57: Leu - Glu(NH<sub>2</sub>) - Gly - Val - Ser - Ileu - Try - Gly - Ser - Gly - Cys - Ala - Glu(NH<sub>2</sub>) - Lys
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the structure of which is discussed in another paper4.

The peptides T-22 (see ref. 1), T-26, T-27, T-45, T-47, T-52, T-56 and T-62 described here apparently coincide with peptides from the tryptic digest of S-sulphotrypsinogen, the full or partial structure of which has been described by WALSH, KAUFFMANN AND NEURATH5.

Peptide T-1 is apparently identical with peptide O-TR-1 as described by DIXON, Kauffman and Neurath⁶; however, according to our analysis the peptide contains two valine residues.

Peptide T-37 apparently represents the N-terminal of the trypsinogen molecule. At this N-terminal is located the well-known "activation peptide" Val-Asp₄-Lys⁷⁻⁹ and into this region most probably fits also the peptide (I)leu-(Gly, Val, Thr, Pro, Cvs. Ala, Asp, Tvr., 5 with the only difference that our peptide T-37 contains three glycine residues. The N-terminal of trypsinogen was formulated by DESNUELLE AND FABRE^{9, 10} and by GABELOTEAU AND DESNUELLE¹¹ as the sequence Val-Asp.-Lys-Ileu-Val-Gly-Glu-Tyr-. According to our analyses the correct formula is that of peptide T-37 which does not contain glutamic acid*.

It further follows from the structures shown here that peptides T-27, T-53 and T-1 represent a part of peptide T-29. As was shown earlier^{1,2}, peptides T-29, T-64, T-24 and T-47 probably follow each other and thus form a sequence of 84 amino acids: Ser-Ala-Tyr-Pro-Gly-Glu(NH2)-Ileu-Thr-Ser-Asp(NH2)-Met-Phe-Cys-Ala-Gly-Tyr-Leu-Glu-Gly-Lys-Asp(NH2)-Ser-Cys-Glu(NH2)-Gly-Gly-Asp-Ser-Gly-Pro-Val-Val-Cys-Ser**-Gly-Lys-Leu-Lys-**Ser-Ala-Ala-Ser-Leu-Asp(NH2)-Ser-Arg-Val-Ala-Ser-(Leu, Ser, Pro, Heu, Thr, Ser, Cys, Ala, Gly, Ala, Ser, Thr, Glu, Cys, Leu)-Ileu-Ser-Giy-Try-Giy-Asp(NH₂)-Thr-Lys-Ser-Ser-Gly-Thr-Ser-Tyr-Pro-Asp-Val-Leu-Lvs. Details of the work described here shall be published in the Collection of Czechoslovak Chemical Communications.

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Since completion of this work, we became aware of the publication in September, 1962, by Walsh et al. 12 in which the N-terminal sequence of trypsinogen is given as: Val-Asp₄-Lys-Ileu-Val-Gly-Gly-Tyr-Thr-Cys-Gly-Ala-Asp₄(NH₂)-Thr-(Val, Pro)-Tyr. The partial structure of our peptide T-37 is in agreement with this.