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The Conformational Potential of Porcine Proinsulin C-Peptide*

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Summary: Statistical analysis of protein sequences lends itself to the identification of regions with a definite inclination to adopt specific main-chain conformations. Application of the model of Chou and Fasman[1,2] to porcine proinsulin C-peptide localizes the tendency to form a helix in the segments (38 to 44) and (51 to 58). A tendency to β turn formation is predicted for the segment (45 to 50). The realization of this conformational potential under native and various other conditions was examined by CD spectroscopy.

Synthetic C-peptide as well as the synthetic fragments (33 - 40), (41 - 52), (41 - 61), (46 - 52), (46 - 61), and (53 - 61) were included in the study. These fragments provide breaks in the amino acid sequence in each of the potentially ordered regions.

The strong helical tendency in the (51 - 58) segment can be activated in the fragments (41 - 61) and (46 - 61) by 1 per cent sodium dodecylsulfate, although the spectrum is not indicative of a classical α-helix. However, the conformation in the (51 to 58) segment should also be non-random in native C-peptide, since cleavage of the (46 - 61) fragment into the subfragments (46 - 52) and (53 - 61) causes considerable spectral effects. Cleavage of the other potentially helical region (38 to 44) between residues 40 and 41, on the other hand, is without spectral consequences. Therefore, this segment is unlikely to be helical in native C-peptide.

In the coherent C-peptide, the helix formation which can be induced by sodium dodecylsulfate in the *C*-terminal part is apparently inhibited by interaction with the *N*-terminal half of the molecule. This interaction implies that the chain is folded back on itself, which is consistent with a high probability of β turn formation in the segment (45 to 50). The CD spectra of the fragments (41 - 52) and (46 - 52), in which the β turn could occur, are characterized by positive ellipticity about 213 nm. The correlation of the β turn with this type of spectrum as well as its definite location are discussed, but cannot be proved solely on CD spectroscopic grounds.

Das Konformationspotential des Proinsulin-C-Peptids vom Schwein

Zusammenfassung: Auf statistisch-analytischem Wege lassen sich in Proteinsequenzen Bereiche identifizieren, die zur Ausbildung bestimmter Hauptkettenkonformationen prädestiniert sind. Die Anwendung des Verfahrens nach Chou und Fasman[1,2] auf das C-Peptid von Schweine-Pro-

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* From the thesis of H.-P. Vogt.