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Tytuł rozprawy doktorskiej: **Synteza oraz badania konformacyjne fragmentów peptydowych tworzących zwroty w wybranych białkach oraz ustalenie sposobu wiązania tych fragmentów białek z jonami Cu(II) i Zn(II).**

Streszczenie w języku angielskim (abstract):

Protein folding is its specific feature and influences its biological activity. The disturbance of this process, which is often the result of a mutation, usually leads to aggregation and the onset of pathological processes. The accumulation of pathological proteins in the body is harmful to nerve cells and most often leads to the development of neurodegenerative diseases.

It is now accepted that the β-turn motif is the primary structural element, which initiates the formation of non-local interactions in proteins and, consequently, the creation of the three-dimensional structure. It has been shown that some short protein fragments can fold in aqueous solutions into conformations with shape similar to that they assume in the parent protein even though they lack fine details such as hydrogen-bonding system.[1] Thus, these fragments may play an important role as nucleation centers in initiating protein folding through local interactions.[2]

The temperature at which the folding process begins and the behavior of the structure at a given temperature turns out to be valuable information in learning about the whole process of protein folding. The pK_a values of the side chains of the charged amino acid residues in the protein are closely related to the shape of its conformation.

The most important information is also the understanding changes of enthalpy of proton dissociation from a system and the sequence of deprotonation reactions of deprotonation of ionizable side groups of amino acid residues in peptides.

The aim of my research in the presented dissertation was to plan and perform the synthesis of selected peptide fragments derived from FBP28, IgG1 and hPin1 proteins. Next, I conducted preliminary structural studies for the compounds obtained using experimental

[1] M. S. Searle, D.H.Williams, L.C. Packman, *Nat Struct Biol*, 1995, 2, 999-1006.

[2] K. A. Dill, *Biochemistry*, 1990, 29, 7133-7155.

methods (circular dichroism, differential scanning calorimetry, potentiometric titration, nuclear magnetic resonance spectroscopy) and molecular dynamics calculation.

An important element of my research was the analysis of acid-base properties of three synthesized hPin1 protein fragments rich in arginine residues separated from each other by several other amino acid residues. I carried out these research using potentiometric titration at three temperatures.

The final stage of my research was to study the interactions of selected protein fragments with metal ions (Cu^{2+} and Zn^{2+}) using isothermal titration calorimetry. On the basis of the obtained data, I determined the thermodynamic parameters of the reactions under study and then, based on these parameters, I determined the dependence of occurrences of interactions between amino acid residues in the peptide and the metal ion.

Research proves that the shape of the β-shift depends strictly on the amount and distribution of the charged amino acid residues in the polypeptide chain, and the conformational equilibrium of the tested compounds is closely related to the temperature.