Level: Bachelor

Course title: Structure and Function of Proteins, B-302

Status: Obligatory

ECTS: 6

Requirements: none

Learning objectives

To provide students with a systematic knowledge of all levels of protein structure and mechanisms of protein synthesis and folding. To enable students to understand the relationship between the three-dimensional structure and biological function of proteins. To familiarize students with main classes of proteins involved in various biological processes. To introduce students to modern techniques used in protein structure determination. To develop students' practical skills in using software for visualization and manipulation of protein models, as well as laboratory skills to carry out Western blot and ELISA methods.

Learning outcomes

Upon successful completion of the course, the student is able to demonstrate systematic knowledge of all levels of protein structure and explain mechanisms of protein synthesis and folding, explain how the three-dimensional structure and reactivity of biological macromolecules determines their biological function, classify proteins according to their function and specify the functions of the main representatives of each class, demonstrate knowledge of the methods used in protein structure determination, independently use software for visualization and manipulation of protein models, and carry out Western blot and ELISA methods.

Syllabus

Theoretical instruction

The primary structure of proteins, sequencing. Non-covalent interactions that stabilize protein structure. Secondary and supersecondary structures. Domains, the tertiary structure. Quaternary structure. Methods for protein structure determination. Translation. Posttranslational modifications. Protein folding. Conformational changes of proteins. Classification of proteins by function. Fibrous proteins. Membrane proteins (ion channels, ion pumps, transporters, receptors). Protein degradation. Immunoglobulins and MHC proteins. Analytical methods based on antigenantibody interactions.

Practical instruction

The acid-base properties of amino acids. Calculation of the ionization state of amino acids and peptides. Calculation of peptides pl. Introduction to databases of proteins and how to use them. Computer practice to master software for visualizing three-dimensional structures of proteins and the analysis of interactions within the protein, the interaction with other proteins, nucleic acids and ligands. The application of NMR and X-ray crystallography techniques in protein structure analysis. Denaturation / renaturation of proteins. The separation of plasma proteins by SDS-PAGE electrophoresis. Western-blot. Application of ELISA methods.

Weekly teaching load				Other:
Lectures: 3	Exercises: 2	Other forms of teaching:	Student research:	