# Proteomics

- Rejuvenation alleviates prolonged postsurgical pain in aging mice by mitigating inflammaging
- DNA-barcode-based Multiplex Immunofluorescence Imaging to Analyze FFPE Specimens from Genetically Reprogrammed Murine Melanoma
- ITGA5 drives glioblastoma progression through SLK-mediated activation of the PI3K-Akt pathway
- Telomere length as a predictive marker for long-term cognitive function in a mouse model of subarachnoid hemorrhage
- In situ incorporation of boronate into carbonized alginate nanogels for targeted inhibition of triple-negative breast cancer metastasis by inducing cytoskeletal disruption, cell growth arrest, and apoptosis
- Quantitative Proteomic Analysis Reveals Different Functional Subtypes among IDH-Wildtype Glioblastoma
- Hyaluronan: An Architect and Integrator for Cancer and Neural Diseases
- Identification of Small Open Reading Frame-encoded Peptides in Glioma by an Optimized Proteomics Strategy

---

Proteomics is the large-scale study of proteins, particularly their structures and functions. Proteins are essential molecules in living organisms, and they play a wide range of roles, from enzymes that catalyze biochemical reactions to structural components in cells and tissues.

Proteomics has numerous applications in various fields, including biology, medicine, and biotechnology. It is used to study diseases, identify potential biomarkers, and develop new therapies. Additionally, proteomic techniques are valuable tools for understanding basic biological processes and the intricacies of cellular function.

Proteomics is the large-scale study of proteins.

The term proteomics was coined in 1997 in analogy with genomics, the study of the genome. The word proteome is a portmanteau of protein and genome and was coined by Marc Wilkins in 1994 while working on the concept as a PhD student.

The proteome is the entire set of proteins,[ produced or modified by an organism or system. This varies with time and distinct requirements, or stresses, that a cell or organism undergoes.

Proteomics is an interdisciplinary domain that has benefited greatly from the genetic information of the Human Genome Project; it is also emerging scientific research and exploration of proteomes from the overall level of intracellular protein composition, structure, and its own unique activity patterns. It is an important component of functional genomics.

While proteomics generally refers to the large-scale experimental analysis of proteins, it is often specifically used for protein purification and mass spectrometry.

## Research

Proteomic research involves the comprehensive analysis of all the proteins present in a specific biological sample or organism. This can include:

Protein Identification: Identifying and cataloging all the proteins in a sample, often done using techniques like mass spectrometry. Mass spectrometry can determine the mass and sequence of proteins.

Protein Quantification: Measuring the abundance of proteins in different conditions or samples to understand their roles and regulation. This can help in identifying proteins that are upregulated or downregulated in response to various factors.

Protein Post-translational Modifications: Investigating the modifications that occur after a protein is synthesized, such as phosphorylation, glycosylation, and acetylation. These modifications can have a significant impact on a protein's function.

Protein-Protein Interactions: Studying the interactions between proteins to understand how they work together in complex cellular processes.

Structural Proteomics: Determining the three-dimensional structures of proteins, which can provide insights into their functions and potential drug targets.

Functional Proteomics: Investigating the functions of proteins in specific biological processes or pathways.

Comparative Proteomics: Comparing the proteomes of different organisms, tissues, or conditions to gain insights into evolutionary relationships or disease mechanisms.

## Cerebrospinal fluid proteomics

Cerebrospinal fluid proteomics.

## Shotgun proteomics

Shotgun proteomics.

## Targeted proteomics

Targeted proteomics.