



## Neuroproteomics: Proteomics Study on Nervous System

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## DESCRIPTION

Neuroproteomics is the study of the proteomes of the nervous system and is crucial for functional research. These proteins work together to influence how the neurons connect, resulting in the intricate structures that are characteristic of the nervous system. The intricate discipline of neuroproteomics still has a ways to go before it can profile the full neuronal proteome. It is a relatively new topic with numerous therapeutic and scientific uses. In order to discover how protein levels, changes, and functions vary after neurotrauma, a new area called neuroproteomics offers a broad-scope, more global examination of protein dynamics. Only a small portion of the neuronal proteome has been mapped thus far, and even then, only when it came to the synapse-related proteins. The four main subcategories of neuroproteomics are :(i)expression neuroproteomics, which is the qualitative and quantitative organising or profiling of neuroproteomes; (ii) functional neuroproteomics, which examines the functional properties of individual proteins as well as their organisation into substructures, complexes, and networks; and (iii) clinical neuroproteomics, which includes the identification of biomarkers and disease; (iv) neuroproteomic informatics, which deals with the analysis of proteomic data sets using computer programmes and databases. Proteins must be differentiated according to the proteome from when they originated for neuroproteomics to work properly. For instance, one group may be under healthy conditions while another may be in unhealthy conditions. Two-dimensional polyacrylamide gel electrophoresis is frequently used to separate proteins (2D PAGE). Techniques for separating proteins, such 2D PAGE, have limitations since they cannot handle protein species with extremely high or low molecular weights. To handle such situations, alternative techniques have been created. These include sodium dodecyl sulphate polyacrylamide gel electrophoresis and liquid chromatography mass spectrometry, as well as multidimensional liquid chromatography mass spectrometry. Neuroproteomics is being used to examine how drug addiction affects synapse function. By isolating specific areas of the brain where synaptic transmission occurs and identifying the proteome for that area, research is being done. Glutamate is released after traumatic brain injury and interacts with ionotropic Glutamate Receptors

(iGluRs). These glutamate receptors cause the cerebral fluid around them to become acidic, further injuring the neighbouring neurons at the molecular level. Neuroproteomics is being used to investigate this cycle, which causes the surrounding neurons to perish through typical apoptosis pathways. Synaptosomes are isolated and functionally intact "nerve endings" that are produced from neurons by mild liquid shear using homogenization in an isotonic sucrose solution. Synaptosome preparation is a common first step in neuroproteomic studies that aim to detect changes in protein expression at the synapse. It is also performed to explore the impact of several proteins on neuritis' early development. It appears that treating each cellular organelle independently will maximise the efficacy of this approach. The development of techniques that will allow for the interrogation of the proteomes of particular populations of the several distinct types of neurons and glia that are present in the mammalian nervous system is a key problem for neuroproteomics, as was described in the introduction. The fact that the brain is made up of many different types of intermixed glial cells and many different types of neurons is perhaps the single biggest barrier faced in most neuroproteomic research. The study of the nervous system's proteome's dynamics and content underlies neuroproteomics. To characterize as many proteins as feasible, the field uses cuttingedge analytical mass spectrometry and cutting-edge highthroughput antibody techniques. Differential analysis has been used most frequently to identify a small number of highly dynamic proteins linked to damage, illness, or other altered states of the nervous system. Neuroproteomics has changed the characterization of protein dynamics in Traumatic Brain Injury (TBI), a significant neurological disorder that has helped us better grasp the post-injury biochemistry. Neuroproteomics has many uses, including the discovery of biomarkers that can be used to assess the severity of an injury, the treatment of the patient, and the result. Through the newly developed techniques of neuroproteomics, a vast number of proteins and their intricate networks spanning various biological activities may be investigated. In the future, neuroproteomic technology willadvance quickly develop to more accurately and effectively identify how TBI has affected the neuroproteome, similar to what the genetic revolution has established

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