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Editorial

# Overview of Neuroproteomics

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## EDITORIAL NOTE

Neuroproteomics is the study of the protein complexes and species that make up the nervous system. In terms of profiling the full neural proteome, neuroproteomics is a complicated field with a long way to go. It is a relatively new topic with numerous therapeutic and scientific uses. Only a limited portion of the neuronal proteome has been mapped thus far, and only when applied to proteins implicated in synapse formation. Marc Wilkins used the term proteomics in 1994 to describe the study of "the protein equivalent of a genome." It is defined as all of the proteins expressed in a biological system at a certain moment under specific physiologic conditions. It can change with any biological change; hence it can only be described in certain circumstances. Neuroproteomics is a subsection of this discipline that deals with the intricacies of neurological disease and its multi-system origins. Because neurological function is reliant on interactions between many proteins of various origins, a comprehensive investigation of subsystems within its proteomic structure is required. When collecting samples, neurologists are mainly interested in a few spots. For neurologists, the plasma membrane is the most crucial place to begin. The vast majority of neuronal transmission occurs here. Because of the large number of raw neuronal proteins to map, initial research must concentrate on small sections of neurons. Ion channels, neurotransmitter receptors, and chemical transporters are among the proteins being mapped. The proteins involved in forming cholesterol-rich lipid rafts throughout the plasma membrane are being researched because they have been demonstrated to be critical for glutamate absorption during the early stages of neuron development.

Proteins must be segregated according to the proteome from whence they came in order for neuroproteomics to work properly. For example, one group may be in normal conditions while the other is in unhealthy conditions. Two-dimensional polyacrylamide gel electrophoresis is routinely used to separate proteins. Proteins are run through an immobile gel with a pH gradient until they reach a point where their net charge is neutral in this procedure. After separating the proteins by charge in one direction, sodium dodecyl sulphate is used to separate the proteins by size in the opposite way.

This technique produces a two-dimensional map that can be used to match other proteins later. Protein separation techniques such as 2D PAGE have limitations in that they cannot handle protein species with extremely high or low molecular weights. Liquid chromatography mass spectrometry in combination with sodium dodecyl sulphate polyacrylamide gel electrophoresis, or liquid chromatography mass spectrometry in several dimensions is examples. Alternative approaches to dealing with similar situations have been created. Liquid chromatography mass spectrometry can handle a wider range of protein species sizes than a basic 2D sheet, but it is limited in the number of protein samples it can handle at simultaneously. The lack of a reference map to work with in liquid chromatography mass spectrometry is also a limitation.

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