First Annual Symposium on Proteome Fractionation

John Hobbs, Guest Editor

In September 2004, the First Annual Symposium on Proteome Fractionation was held at Harvard University, Cambridge. MA. The presentations mainly dealt with the application of multidimensional techniques to the fractionation of various proteomes. As the field of what is now referred to as proteomics has developed, it has become increasingly apparent that traditional separation technologies were not sufficient to dissect proteomes in adequate detail and that new advances were needed. The use of multidimensional techniques offers considerable promise to help meet these needs, and their use has increased markedly over the past few years. This symposium presented some current applications in diverse areas of research where this approach has played a major role in the discovery process.

The application of multidimensional chromatography to proteomics is not a new phenomenon; however the introduction of the ProteomeLab™ PF 2D concept takes what can be a complicated process requiring specialist skills and makes it usable on a routine basis by non-chromatographers. Automated hardware, pre-optimized chemistry, and simple visualization software that generates a proteomic "map" are combined to provide a standardized approach for protein fractionation and comparison of proteome profiles. Chromatofocusing is used for the first dimension, resulting in fractionation according to the pI of the proteins. The fractions from the first dimension are automatically injected into a reversed phase system where proteins are fractionated according to their hydrophobicity. The use of solid microparticles in this dimension results in highly efficient, fast separations. The end result is a series of liquid fractions containing proteins in solution, making subsequent analysis, using mass spectrometry, for example, a relatively simple matter.

Using this approach as part of a "divide and conquer" strategy has led to the identification of proteins previously not found in certain proteomes. The range of proteomic applications presented at the symposium displayed the versatility and potential of this approach and is illustrated by the several articles found in this issue taken from that program.