Award for a Distinguished Contribution in Mass Spectrometry

William J. Henzel, John T. Stults, Colin Watanabe

The Distinguished Contribution Award recognizes a focused, singular achievement in or contribution to fundamental or applied mass spectrometry. The 2002 award is presented to **William J. Henzel, John T. Stults,** and **Colin Watanabe** of Genentech, South San Francisco, California, for the initial implementation of peptide mass fingerprinting for the rapid identification of protein components. The use of peptide mass maps for sequence database searching was proposed in 1989, and is now widely practiced. The initial method utilized a computer program, FRAGFIT, that identified a protein by matching two or more molecular masses of peptide fragments obtained from chemical or enzymatic cleavages with fragment masses in a protein sequence database. At that time, fast atom bombardment (FAB) and plasma desorption mass spectrometry were the most common ionization methods for analysis of peptide mixtures. The results of the initial demonstration were presented as a poster at the Third Symposium of the Protein Society in Seattle in August 1989. This methodology was the first to allow protein identification without the need for time-consuming Edman sequencing or immunoaffinity probes.

In the early 1990s, this team improved the methodology ...ssed even further owing to contemporaneous advances in matrix-assisted laser desorption ionization time-of-flight (MALDI-...ectrometry. Their landmark study reported in 1993 in the Proceedings of the National Academy of Sciences USA (volume 90, ...incingly showed that MS approaches alone could be used to analyze proteins from two-dimensional polyacrylamide gels. ...ments by a number of researchers, including the completion of a number of genome sequences, the incorporation of MS/MS ...ing, and improvements in sensitivity, mass accuracy, and sample throughput have made this the method of choice for the ... proteins from gels. This methodology is a key component that links mass spectrometry to post-genome biology. It is used ...laboratories around the world. Its importance is further seen by the number of databases available for mass-based searches, ...s presence of sequence database search engines supplied with commercial mass spectrometer data systems. The ability to ... proteins from complex samples has led to the field of proteomics.

...m J. **Henzel** began his career in protein chemistry at the Department of Immunology at Boston Children's Hospital/Harvard ... Later, he moved to the University of Massachusetts before joining Genentech. **John T. Stults** received a B.A. in Chemistry ...ge of Wooster in Wooster, Ohio. His Ph.D. in Analytical Chemistry was obtained from Michigan State University with ... Professors Christie G. Enke and Jack Throck Watson. **Colin Watanabe** obtained his B.S. and M.S. degrees in Chemical ...from the University of California, Los Angeles. Currently, he is a Distinguished Software Engineer at Genentech.

The Biemann Medal

Ruedi Aebersold

The Biemann Medal recognizes a significant achievement in basic or applied mass spectrometry made by an individual early in his or her career. The 2002 medal is presented to **Dr. Ruedi Aebersold**, Institute for Systems Biology, for his achievements and contributions to areas of biological mass spectrometry, analytical biochemistry, and biology.

Dr. Aebersold has been a key contributor to the development and application of mass spectrometry for the identification and characterization of proteins. He developed sensitive methods for direct N-terminal and internal sequencing of polyacrylamide gel-separated proteins. He has made important contributions to the development of LC-MS, LC-MS/MS, and capillary electrophoresis-MS for peptide mapping and protein identification. He has also been at the forefront of research for the characterization of protein phosphorylation. Dr. Aebersold has developed very rapid, ultrasensitive mass spectrometric methods for phosphorylation site mapping and is making singular contributions to the field of signal transduction. He has been instrumental in the development of microfabricated instrumentation for ultrasensitive mass spectrometry of proteins. Most recently, Dr. Aebersold has developed a method for accurately quantifying variations in the levels of proteins in cells as changes are made to the cellular environment and to the genome itself. Multidimensional chromatography of the complex peptide mixtures generated by the digestion of unseparated protein samples has been introduced for the identification of their components, and isotope-coded affinity tags (ICAT) have been introduced to allow for accurate ... of the components of protein mixtures by mass spectrometry. The ICAT method, reported in his 1999 publication in Nature ... volume 17, page 994), may be the key step to making mass spectrometry the tool of choice for protein expression mapping ...teomics studies.