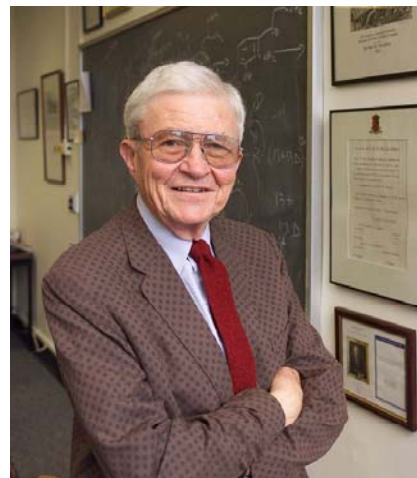


IAPSAP/MPSA 2006 Pehr Edman Awards

The 2006 IAPSAP/MPSA Pehr Edman Awards will be presented to Dr. Fred W. McLafferty, Cornell University, Professor Emeritus, and Dr. Darryl Pappin, Advanced Research and Technology division of Applied Biosystems. The awards are supported by Applied Biosystems, Inc. and Agilent Technologies.

Dr. McLafferty received his BS (1943; U.S. Army Infantry, 1943-5, France and Germany) and MS (1947) from the University of Nebraska and PhD from Cornell University. At the Dow Chemical Company, he was in charge of mass spectrometry and gas chromatography (1950-6) and was director of their Eastern Research Lab for basic research. He moved in 1964 to Purdue University and in 1968 to Cornell (Peter J. W. Debye Professor of Chemistry, Emeritus). He is a member of the U.S. National Academy of Sciences (1982), American Academy of Arts and Sciences (1985), and the Italian Academy of Sciences XL (2002). He has been a mass spectrometry pioneer in such fields as gaseous ion reactions (McLafferty rearrangement), instrumentation (GC/MS, LC/MS, MS/MS), techniques (collisionally activated dissociation, neutralization-reionization, electron capture dissociation, IR photodissociation spectroscopy), computer data acquisition, reduction, and identification (Probability Based Matching), and reference data (600K mass spectra). His more recent work concerns MS/MS and IRPDS characterization of biomolecules ("top down" proteomics) and gaseous protein conformers.



Dr. Pappin received his BSc (1977) and PhD (1984) from the University of Leeds (UK). In 1987, he moved to Millipore in the US, working on the development of instruments and membrane-based supports for solid-phase Edman sequencing. In 1990 he took up a position at ICRF (now CRUK) in London as head of the Protein Sequencing Laboratory. In 1997 he was made an honorary Reader in Biochemistry and Molecular Biology at University College, London, and in 2000 was appointed Professor of Proteomics at Imperial College. At ICRF, he was an early pioneer in the development of computer programs for the identification of proteins by peptide-mass fingerprinting, and developed the MOWSE and MASCOT search engines and the MSDB protein sequence database. He also developed methods for peptide ladder sequencing using volatile isothiocyanates and explored chemical tagging approaches for directing and simplifying peptide CID spectra. At Imperial, he began development of the iTRAQ isobaric mass tag reagents for protein quantitation. In 2002 he returned to the US, and is currently a

Scientific Fellow in the Advanced Research and Technology division of Applied Biosystems.

The Pehr Edman Award is given to individuals whose efforts have significantly advanced the fields of protein chemistry, protein structure analysis, or proteomics. The award honors and commemorates the work of Pehr Edman, the Swedish chemist principally responsible for

developing the chemistry for sequencing proteins by removing amino acids from the amino terminus one at a time. The Award is given in conjunction with Methods in Protein Structure Analysis (MPSA) meetings, which are sponsored by the International Association for Protein Structure Analysis and Proteomics (www.iapsap.bnl.gov). The first prize was awarded to Richard Laursen in 1988 for his efforts in the development of solid-state protein sequencing methods. In 2002, the award was given to Professor Hans Jörnvall, Karolinska Institute, Stockholm, Sweden, for contributions to protein chemistry, structure and function through the development of techniques associated with the use of Edman chemistry and structure function studies on alcohol dehydrogenases, and to Professor Kenneth Walsh, University of Washington, Seattle, Washington, USA for his contributions to the development of mass spectrometry for characterizing the chemical structure of proteins and their posttranslational modifications and for concepts contributing to the evolution of protein structure and function. In 2004, Dr. Stephen Altschul, of the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, USA, was honored for his contributions to the field of protein sequence comparison and analysis and his role in developing the BLAST and PSI_BLAST sequence database search programs. Dr. Amos Bairoch, of the Swiss Institute for Bioinformatics, Geneva, Switzerland was also honored for his work in in the field of protein sequence analysis and the development of databases and software tools for the analysis of proteins. He is best known for the development and maintenance of the Swiss-Prot database, the best known and most widely used database on proteins.