Dr. Robert J. Cotter is Professor of Pharmacology and Molecular Sciences at the Johns Hopkins University School of Medicine.

Tandem mass spectrometry (MS/MS) is a key tool for molecular structure elucidation. Many instrument configurations are feasible for accomplishing gas-phase analyte selection followed by activation and molecule-specific dissociation. Robert J. Cotter is recognized for his invention and development of tandem time-of-flight (TOF/TOF) mass spectrometry that utilizes high-energy collisions (up to 20 keV) for collision-induced dissociation. Cotter's first instrument design, realized in 1993, incorporated two dual-stage reflectrons (rTOF/rTOF), which were later replaced by single-stage reflectrons for improved focusing of product ions over a wider mass range. This work was followed by the development of the “curved-field reflectron” to enable simultaneous focusing of the entire product ion mass range. The curved-field reflector also gained wide use on post-source decay instruments and was licensed to Kratos Analytical for their Kompack IV, AXIMA CFR and AXIMA CFR+ mass spectrometers and then Shimadzu Confidence mass spectrometers. A simplified instrument configuration, developed in 2004, was commercialized as the Kratos AXIMA TOF, and later the Shimadzu Performance. More than 400 curved field reflectron instruments have been manufactured and sold. The potential benefits of high-energy (20 keV) collisions are now being appreciated, with perhaps the most exciting being the possibility of carrying out “top-down” or “middle-down” protein analyses on a MALDI TOF mass spectrometer.

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Dr. Béla Paizs is Group Leader, Gas-phase Peptide Chemistry Group at the German Cancer Research Center.

Tandem mass spectrometric analysis of peptides, a vital element of proteomics, requires a deep understanding of the complex fragmentation reaction networks occurring in mass spectrometers under various excitation conditions. The focused efforts of Béla Paizs have led to detailed characterization of peptide product ion structures and dissociation mechanisms, and have demonstrated that the principle characteristics of peptide collision-induced dissociation spectra can be understood with basic physical and chemical laws. Paizs’ work combines various experimental techniques (e.g., MS/MS, “action” infrared multiphoton dissociation, ion mobility spectrometry, gas-phase H/D-exchange) with state-of-the-art theoretical methods. “Raw” experimental data (fragmentation patterns, IR spectra, collision cross-sections, etc.) are processed with the help of advanced modeling and provides invaluable structural, thermodynamic, and kinetic data on peptide fragmentation chemistry. Among other achievements, Paizs has characterized the major fragmentation pathways leading to $b$, $y$, and $a$ ions, the scrambling chemistry of $b$ fragments, and very recently, he has described a new rearrangement pathway for $a$ fragments. His work has unified diverse dissociation mechanisms into a comprehensive peptide fragmentation model. These achievements have substantially advanced the field of peptide characterization and provide a solid scientific background for developing improved bioinformatics tools for peptide sequencing in mainstream proteomics.

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The Ron Hites Award recognizes an outstanding presentation of original research. Selection is based on a paper's innovative aspects, technical quality, likely stimulation of future research, likely impact on future applications, and quality of presentation. The award is named in honor of Professor Ronald A. Hites of Indiana University, who led the creation of JASMS in 1988 while president of ASMS.

The 2011 award is presented to Prof. Scott A. McLuckey for the article “Top-Down Tandem Mass Spectrometry of tRNA via Ion Trap Collision-induced Dissociation;” Huang, T.-Y., Liu, J., & McLuckey, S. A.; JASMS 2010, Vol. 21(6), 890-898. Prof. McLuckey is in the Department of Chemistry, Purdue University. Prof. McLuckey is donating the award prize of $2,000 toward student travel support.