When she joined the faculty of the Department of Pharmacology and Experimental Therapeutics at the Johns Hopkins School of Medicine in 1967, Catherine Fenselau (Cotter) was given the job description to develop and exploit mass spectrometry’s new high mass, high resolution capabilities across the spectrum of biomedical research. Peptide and protein analysis held her attention from the beginning. In 1982 the Hopkins laboratory published the first considerations of the isotopic complexities of protein molecular ion populations. In 1992 her team, now at UMBC, produced the first experimental measurement of the proton affinity of arginine, a major determinant of peptide fragmentation. Mass spectrometry and HPLC-based studies of protein acylation by carboxyl-linked glucuronides, stoichiometric metal ion flux in metallothionein, site-specific alkylation of metallothionein by therapeutic agents, modifications and processing of the HIV GAG protein, and many others positioned her to be an early contributor to the global post-genomic effort now known as proteomics. Several highlights can be mentioned. In 2001 her group at the University of Maryland showed that differential quantitation could be achieved in bottom-up proteomic strategies by implementing trypsin-catalyzed 18O-labelling. More recently they were the first to demonstrate the reliability of label-free quantitation in top-down LCMS analysis on the proteome scale. They worked out novel top-down strategies to identify internally and terminally truncated proteoforms in proteomic samples and to attack the challenging structural analysis of branched proteins -- unanchored polyubiquitins and ubiquitinated proteins. A decade-long collaborative study of the protein and small RNA cargos of the exosomes shed by myeloma-derived suppressor cells has made significant contributions to understanding the mechanisms by which the immune response is suppressed in the tumor microenvironment.

Dr. Fenselau has trained more than 150 new investigators in research projects supported by competitive funding from the NIH, NSF, WHO, DOD and private foundations. Her bibliography lists more than 400 peer reviewed research papers, book chapters and editorials. Her discoveries and contributions in mass spectrometry, pharmacology, rapid microorganism detection, and proteomics have been recognized by many scientific awards and she has contributed to the academic and international scientific communities in both committee work and leadership positions. She was a founding member of International HUPO, a founding member of US HUPO, and a founding editorial advisor of the Journal of Proteome Research.