

Michael MacCoss, PhD: Michael MacCoss has been working with mass spectrometry instrumentation since 1994 when he was an undergraduate at the University of Vermont. He became interested in biomedical applications working in Dr. Patrick Griffin's protein mass spectrometry lab at Merck Research Laboratories during two summer internships in 1995 and 1996. In 2001, he completed a Ph.D. in Analytical Chemistry with Professor Dwight Matthews in the development of stable isotope and mass spectrometry methodologies for the measurement of human amino acid and protein metabolism. After completing his degree, Dr. MacCoss moved to The Scripps Research Institute to work with Professor John R. Yates III as a postdoctoral fellow. Dr. MacCoss moved to the University of Washington in 2004 as faculty member in the Department of Genome Sciences, where his lab has focused on the development and application of mass spectrometry-based technologies for the quantitative characterization of complex protein mixtures. The MacCoss laboratory has been actively applying these tools to important areas of biology including but not limited to, the basic biology of aging, protein-protein interactions, measurement of protein half-life, transcriptional regulation, proteogenomics, and clinical diagnostics. Our laboratory is widely known for its expertise in the development and support of proteomics software tools.