

Tim Griffin, PhD: Dr. Griffin's research involves the development and application of mass spectrometry-based tools for systems biology applications. On the technology side, he maintains an interest in developing new methods (analytical and computational) for enabling more sensitive and accurate mass spectrometry-based proteomic and metabolomic studies in complex biological systems. Via his role as Faculty Director of the Center for Mass Spectrometry and Proteomics (CMSP) he facilitates collaborations with numerous research laboratories, bringing advanced sample processing, instrumentation and computational tools to bear on important biological research questions – for proteomic and metabolomics applications. Dr. Griffin has led research (funded by both the NIH and NSF) seeking to develop bioinformatics tools for multi-omics, with a focus on integrating mass spectrometry-based proteomics and metabolomics data with genomic data types. This ongoing project (called the Galaxy-P project, galaxyp.org) extends the popular Galaxy platform for new applications in proteomics and other 'omic areas. Part of this work focuses on proteogenomics (<http://galaxyp.org/proteogenomics/>), which integrates genomic and proteomic data to sequence proteins, immunopeptides and other variants arising from mutations. Other applications include the emerging area of metaproteomics, seeking to identify proteins expressed by microbiota that play a role in host cancer development and progression.