Unlocking a deeper understanding of how proteins function within the human body underlies the mission of Northwestern Proteomics. Although the completion of the Human Genome Project in 2002 transformed our knowledge of the role that genetics plays in the scientific makeup of humans, studies now point to proteins, not genes, as the main drivers of human health and complex diseases. When proteins change or confront a challenging environment, disease becomes more likely.

Northwestern Proteomics is at the forefront of the Human Proteoform Project (HPfP), a game-changing initiative to identify all one billion proteoforms present in all types of human cells and fluids. Integral to the project is the Human Proteoform Atlas, a database, developed and hosted by Northwestern Proteomics, that provides a central location for scientists to browse proteoforms and contribute their own datasets. The goal of this ambitious undertaking is to reveal why proteins follow or diverge from their biological instructions and to make possible more precise identification of disease types. These critical insights will accelerate the development of more targeted and effective diagnostics and treatments with the potential to revolutionize personalized medicine.

Northwestern Proteomics, a Center of Excellence within the Chemistry of Life Processes Institute (CLP), is the leading lab in the world for the top-down proteomics approach. Neil L. Kelleher, PhD, Walter & Mary E. Glass Professor of Molecular Biosciences, Professor of Chemistry, and Professor of Medicine, and Director of Northwestern Proteomics and CLP, has been successful in driving both technology development and applications of very high-performance mass spectrometry in chemistry and biology. For almost 20 years, he has worked to develop an innovative a set of tools and methodologies to identify proteoforms, or specific molecular forms of a protein product, arising from a specific gene.

Most proteomics researchers are attempting to determine the composition of proteins and identify their role in determining diseases through a bottom-up approach that breaks down proteins into small units to partially analyze. This approach, however, is incomplete. Kelleher and his team have pioneered a groundbreaking new method for measuring intact proteins in the mass spectrometer known as top-down proteomics. It offers tremendous insight into the proteoforms which are associated with health outcomes or particular diseases.

Kelleher is the international leader in his field and founding president of the Consortium for Top-Down Proteomics, a 350-member organization with global reach.

Pushing the Boundaries of Science

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Core Facility

Northwestern Proteomics partners with more than 100 Northwestern labs on the Chicago and Evanston campuses. In the last four years, the Center has interacted with nearly 200 Northwestern investigators, ranging from simple, core work to deep, long-term collaborations.

Our research faculty and core facility staff are experts in technology development for complex sample analysis using liquid chromatography mass spectrometry for untargeted and targeted applications in proteomics and metabolomics.

Our proteomics core facility performs both traditional bottom-up proteomics, where proteins are digested with an enzyme prior to analysis and intact, top-down proteomics analyses. These experiments lead to protein identification to protein quantitation (both relative and absolute).

Our goal is to develop new proteomics technologies, apply them to timely questions in basic, translational, and clinical research, and educate the scientific community at large about our research findings.