14 Gill Street, Unit H
Woburn, MA, USA
Phone: +1 781-9323959

Ensuring High Quality Data with a Robust Comprehensive Sample Preparation Workflow

The advancement in detection technologies have changed the landscape of Omics where Proteomics now play an extremely important role. From the academic researchers focused on global proteomic studies to Biomarker identification and monitoring; from looking at endogenous proteins to design, develop and monitor a certain protein based biotherapeutic through a human system –proteins continue to be an extremely important target, marker, and approach. However, protein analysis is also laced with several analytical challenges that are addressed by the labs, every day. The root of the complex challenges are typically defined by inefficient sample processing and lack of standardization.

As mentioned above, advancements in the end-detection technology for proteins (such as, LC-MS) have been significant over the last decade. However, when it comes to injecting good quality samples to the LC, a reasonably good sample preparation workflow can be found for a few types of samples, and not for every matrix type.

Covaris' comprehensive, robust, reliable protein analysis workflow solutions enabled by the class-leading Adaptive Focused Acoustics® (AFA®) Technology offer every laboratory a unique opportunity to confidently extract, isolate/purify proteins and digest to peptides with remarkable efficiency and speed – higher than ever before. In this regard, Covaris' workshop at the DGMS meeting will focus on highlighting several key applications that capitalize AFA en route to a comprehensive sample preparation workflow that offers efficient extraction, reliable purification (using a class leading protein aggregation capture protocol), and accelerated digestion for proteins from any sample matrix. From mammalian cells to fresh frozen tissues, from FFPE to plasma – every matrix can be addressed, regardless of the number of proteins, user expertise, and complexity of proteins. A detailed discussion on different sample matrices, different protein groups and workflows would help you understand the benefits of capitalizing Covaris protein analysis sample preparation workflow.

Covaris®

14 Gill Street, Unit H
Woburn, MA, USA
Phone: +1 781-9323959

Deb Bhattacharyya received his Master of Science in Chemistry from Indian Institute of Technology (Mumbai, India) and his PhD in Chemistry and Biochemistry from Emory University (Atlanta, GA, USA). From his doctoral studies to his stint as a Research Associate at the University of North Carolina – Chapel Hill, Deb's research work in Oncology focused on high-definition structural elucidation of Protein-DNA and Protein-Protein complexes in cancer research. In his professional career spanning more than 17 years in biotechnology, Deb has worked for several Mass Spectrometry manufacturing organizations focused on designing, developing, and optimizing workflows on proteomics, biomarker, and biotherapeutic characterization and quantitation. Deb has also been instrumental in launching several MS instruments and LC-MS based workflows that has helped many organizations achieve success in their protein analysis workflows.

At Covaris, Deb is the Vice President of Business Development and Emerging Markets and capitalizes his expertise and experience in expanding Adaptive Focused Acoustic® (AFA®) Technology's capabilities in multi-omics comprising Genomics, Epigenomics, Proteomics, and Metabolomics. Deb has authored/co-authored more than 50 articles on varied topics and applications ranging from cancer research to forensic toxicology, clinical research to biopharma.