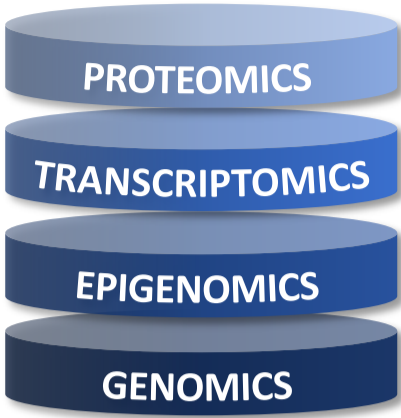


Seminar title: Adaptive Focused Acoustics Technology Enabling Multi-Omics Approach in Precision Medicine

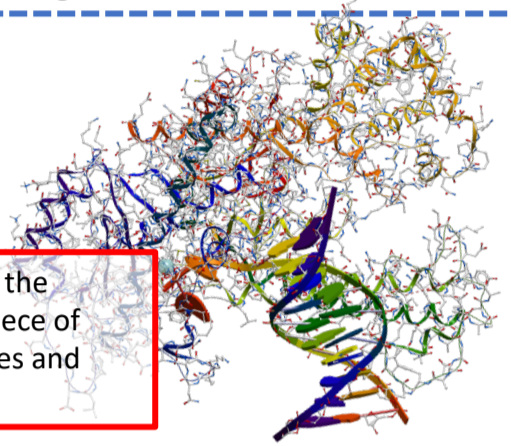
Where: March 28, 2023, from 12.30 to 1.30 PM

When: Chemistry and Materials Building, conference room 201

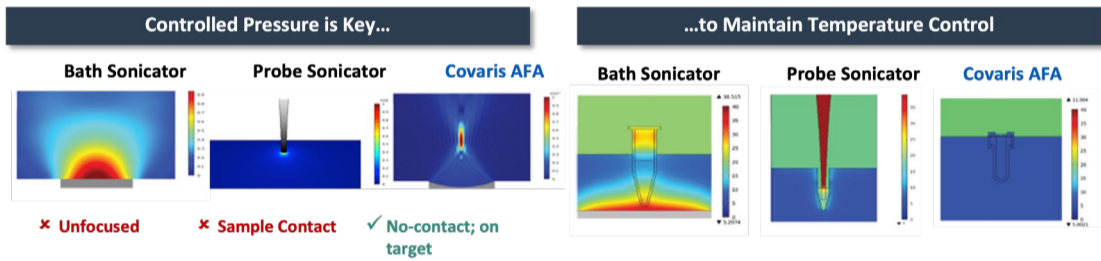
MultiOmics Enabled by AFA® Technology



Connecting genotype to phenotype means combining DNA, epigenetics, RNA, protein, or other molecular measurements into a full cellular readout provides researchers with novel scientific insights that cannot be found from single omic methods alone.

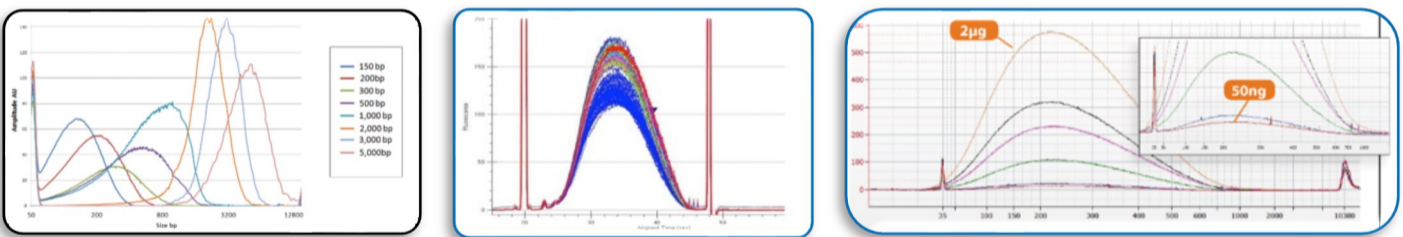


Bigger picture with MultiOmics—MultiOmics goes beyond the genome to unlock deeper biological insights. Using every piece of molecular data available can accelerate biological discoveries and transform our understanding of human health.

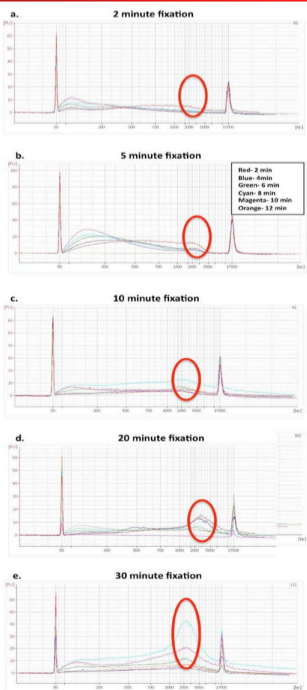


AFA employs highly controlled bursts of focused high-frequency acoustic energy to efficiently and reproducibly process samples in a temperature-controlled and non-contact environment.

Gold Standard for DNA Shearing Enabling Comprehensive Genomic Profiling

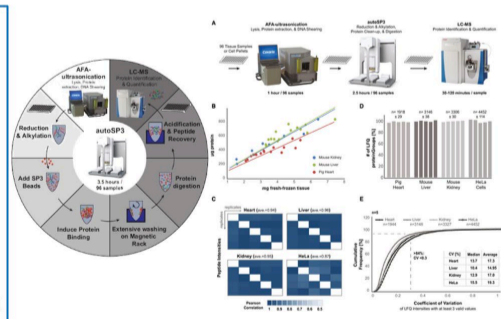


Chromatin Shearing with AFA



Proteomics Sample Prep with AFA

- Sample preparation in proteomics largely relies on manual handling
- Seamless integration of these steps into an automated process (autoSP3 + AFA) removes shortcomings
- High reproducibility across different tissue types and steps
- Handle detergents, including SDS, adds great flexibility
 - Efficient lysis of fresh and FFPE tissue (1 and 4% SDS) without the need for further peptide clean-up before LC-MS
- Fast workflow (3.5 h for 96 samples (1 h for ultrasonication, 2.5 h for autoSP3)) up to digestion
 - Allows for processing 2-3 plates (or up to 300 samples) per working day with minimal hands-on time



Metabolomics Sample Prep with AFA

Combining Proteome and Metabolome Analysis in Plasma/Serum

- Metabolomic and proteomic analyses of human plasma and serum samples harbor the power to advance our understanding of disease biology.
- Pre-analytical factors may contribute to variability and bias in the detection of analytes, caused by sample handling, processing time, and different procedures
- Targeted metabolic profiling (497 metabolites) and proteomics (572 proteins) on the same samples revealed time and temperature as the strongest influencers
 - Rapid handling and low temperatures (4°C) are imperative for metabolic profiling
 - Proteome showed variability at 4°C for more than 2 hours
- Robust quality control scoring system was developed for evaluation of sample stability

