NEWOMICS
Enabling Precision Medicine

Newomics Breakfast Talks at ASMS 2022

When: Tuesday, June 7 at 7 am CT
Where: Room 200J

Talk 1: *Simion Kreimer, Ph.D., Cedars-Sinai*

Maximizing Throughput with Parallelization in Rapid Proteomic Analysis of Large Sample Sets

Epidemiological biomarker cohort studies and in-depth cell-based perturbation studies require high throughput to appropriately capture population and biological heterogeneity over thousands of samples. To achieve this, a short liquid chromatography gradient paired to rapid mass spectrometry data acquisition can be used to reproducibly profile a moderate set of analytes. High throughput profiling at a limited depth is becoming an increasingly utilized strategy for tackling large sample sets but the time spent on loading the sample, flushing the column(s), and re-equilibrating the system reduces the ratio of meaningful data acquired to total operation time (instrument utilization, IU). The goal is to maximize IU and consequently the number of quantified analytes during short analysis times. The dual-trap single-column configuration presented here maximizes IU in rapid analysis (15 min per sample) of blood and cell lysates through parallelization of trapping column cleaning and equilibration and sample loading and desalting with analysis of the previous sample. We achieved 90% IU in low micro-flow (9.5 uL/min) analysis of blood while reproducibly quantifying 300-400 protein groups and over 6000 peptides. The same IU was achieved for cell lysates, in which over 4,000 proteins and 40,000 precursor ion were quantified at a rate of 15 minutes/sample.

Talk 2: *Rebekah Gundry, Ph.D., University of Nebraska Medical Center*

Multi-nozzle emitters for structure-based glycomics

Glycans play critical roles in physiology and disease. MS-based methods can reveal both composition and structure of glycans. This knowledge is invaluable in diverse contexts spanning across biologic drugs to novel biomarkers of health and disease. Both biomarker discovery and the characterization of biologics would benefit from robust and sensitive LC-MS/MS methods for structurebased glycomics analyses. While microflow methods are typically more robust and easier to implement for higher throughput analyses, they are less sensitive than nanospray methods. Nanospray methods offer higher sensitivity, but are often less robust. Here, we evaluated the Newomics™ MnESI source and M3 emitters for increased sensitivity of a microflow method for robust, high throughput structure-based glycomics analysis. From 2 μL of serum or one FFPE slide, hundreds of N- and O-linked glycan structures were identified over 5 orders of magnitude of abundance. Compared to the traditional electrospray source, the M3 emitters resulted in a 4-10 fold increase in signal intensity for known glycans. Additionally, from the same amount of starting material, >50 glycan structure isomers were detected only when using the M3 emitters. Coupling the M3 emitters to 200 μm in-house packed PGC columns, glycan signals from serum samples were stable for >4 weeks of continuous data acquisition (>400 injections). This setup is overall well-suited to high throughput analysis of glycan structures for biomarker studies and analysis of biologics.