



Medium Depth High Throughput Proteomics Profiling using dia-PASEF for agricultural and biological fluid applications in a core facility

Brett Phinney

Ph.D., Director Proteomics Core, Genome Center, University of California, Davis, CA, USA

The advent of Data independent Acquisition, deep learning and fast scanning/sensitive mass spectrometers has dramatically increased the number of proteins that can be quantified using shorter run times and more robust larger columns. For many applications it is advantageous to increase your N vs your depth. I will present a few examples of how we do this using diaPASEF in an academic core facility to increase the number of samples we can analyze while decreasing instrument time.