



Affinity-Bead Assisted Mass Spectrometry (Affi-BAMS): A Multiplexed Microarray Platform for Targeted Proteomics

Ghaith Hamza

AstraZeneca, BioPharmaceuticals R&D, Discovery Science

Proteomic studies often employ multi-dimensional analytical methods such as nano-LC-ESI-MS/MS to simplify the sample complexity of target peptides within a biological sample of interest. In this presentation, we will describe a versatile microarray assay platform called Affinity-Bead Assisted Mass Spectrometry (Affi-BAMS™) that integrates immuno-affinity capture with MALDI MS detection for carrying out multiplexed, LC-free targeted proteomics. The Affi-BAMS™ platform supports targeted assays to specific proteins and/or protein post-translational modifications (PTMs) for simultaneous, multiplexed profiling for bottom-up, middle-up and top-down proteomic applications. The workflow combines antibody enrichment of target analytes onto individual magnetic Affi-BAMS™ beads, which are arrayed in temporary microwells for localized elution for subsequent MALDI MS (or MS/MS) measurement.

During this webinar, I will review the basic principles of Affi-BAMS™ including the method workflow, the assay components and the assay panel validation process. In addition, I will highlight several different targeted proteomic applications utilized to support the drug development/discovery efforts at AstraZeneca.