



Bead Assisted Mass Spectrometry (BAMS™) for Targeted Proteomics: Single Bead Multiplexed Immunoassay Platform with MALDI MS Detection

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Bio: Dr. Jeffrey Silva got his Master's and Ph.D. in Chemistry from Johns Hopkins University studying natural product biosynthesis and secondary metabolism in fungi, to examine how aflatoxin is produced by *Aspergillus parasiticus*. After graduate school he pursued his post-doc at Harvard Medical School studying prokaryotic signal transduction of the model, two-component systems, PhoBR and VanRS. After that, he transitioned to industry working as a senior scientist at a start-up company called Microbia (currently known as Ironwood Pharmaceuticals) focusing on Bioengineering fungal secondary metabolism and signal transduction machinery to overproduce pharmaceutically relevant natural products. After Microbia he spent many years working at Water Corporation as a development scientist in the area of global proteomics using novel LCMS methods. He later joined Cell Signaling Technology, where he served as the Director of the Proteomics Service Group, integrating affinity capture with mass spectrometry to carry out quantitative proteomics in the areas signal transduction (Serine, Threonine and Tyrosine phosphorylation), ubiquitin-directed protein degradation, as well as protein methylation and acetylation. He joined Adeptrix Corporation in 2017 and serves as the Chief Technology Officer to introduce a new assay technology platform that combines single-bead immunoaffinity capture with MALDI mass spectrometry for a wide range of targeted proteomic applications. He has also served as an Advisory Board Member at the Life Sciences Consortium of the North Shore, and a member of the Education Advisory Council at the Gloucester Marine Genomic Institute and their Biotechnology Academy.