

4th World Congress on

MASS SPECTROMETRY

June 19-21, 2017 London, UK

Integrated microfluidics for protein modification discovery

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Protein post-translational modifications mediate dynamic cellular processes with broad implications in human disease pathogenesis. There is a large demand for high-throughput technologies supporting post-translational modifications research, and both mass spectrometry and protein arrays have been successfully utilized for this purpose. Protein arrays override the major limitation of target protein abundance inherently associated with MS analysis. This technology, however, is typically restricted to pre-purified proteins spotted in a fixed composition on chips with limited life-time and functionality. In addition, the chips are expensive and designed for a single use, making complex experiments cost prohibitive. Combining microfluidics with *in situ* protein expression from a cDNA microarray addressed these limitations. Based on this approach, we introduce a modular integrated microfluidic platform for multiple post-translational modifications analysis of freshly synthesized protein arrays (IMPA). The system's potency, specificity and flexibility are demonstrated for tyrosine phosphorylation, auto-phosphorylation, and ubiquitination in quasi-cellular environments. Unlimited by design and protein composition, and relying on minute amounts of biological material and cost-effective technology, this unique approach is applicable for a broad range of basic, biomedical and biomarker research.

Biography

Amit Tzur has completed his PhD at Hebrew University of Jerusalem, Israel and his Post-doctoral training at Harvard Medical School, Boston MA. He is an Assistant Professor at Bar Ilan University, Israel, and a member of the Bar Ilan's Institute of Nanotechnology and Advanced Materials (BINA) and Israel Center of Excellence (I-CORE). His research focuses on "Physiology and molecular dynamics of proliferating cells". He has published dozens of papers in reputed journals and serving as an Editorial Board Member.

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