

# Protein Microarray: “Theory” to “Real Practice”

Ng Jin Kiat<sup>1</sup>, PARAYIL Kumaran Ajikumar<sup>1</sup>, Lee Jim Yang<sup>1,2</sup>, Gregory Stephanopoulos<sup>1,3</sup>,  
Too Heng-Phon<sup>1,4</sup>

<sup>1</sup>MEBCS, Singapore-MIT Alliance, 4 Engineering Drive 3, National University of Singapore, Singapore-117576, <sup>2</sup>Chemical and Biomolecular Engineering, National University of Singapore.; <sup>3</sup>Department of Chemical Engineering, Massachusetts Institute of Technology; <sup>4</sup>Department of Biochemistry, Kent Ridge Crescent, National University of Singapore

**Abstract** – Fueled by ever-growing genomic information and rapid developments of proteomics—the large scale analysis of proteins and mapping its functional role has become one of the most important disciplines for characterizing complex cell function. For building functional linkages between the biomolecules, and for providing insight into the mechanisms of biological processes, last decade witnessed the exploration of combinatorial and chip technology for the detection of biomolecules in a high throughput and spatially addressable fashion. Among the various techniques developed, the protein chip technology has been rapid. Recently we demonstrated a new platform called “Spatially addressable protein array” (SAPA) to profile the ligand receptor interactions. To optimize the platform, the present study investigated various parameters such as the surface chemistry and role of additives for achieving high density and high-throughput detection with minimal nonspecific protein adsorption. In summary the present poster will address some of the critical challenges in protein micro array technology and the process of fine tuning to achieve the optimum system for solving real biological problems.