

TITLE

**Single cell
proteomics on
a multiplexed
nanosystem platform**

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Cells in a tumor usually respond differentially to either conventional chemotherapy or targeted drug treatment, which leads to failure of cancer therapy. Thus, biological information from single cells is highly demanded in consideration of heterogeneity of a tumor sample. However, function assay of single cells through proteome profiling in a large population has been extremely difficult due to low abundance of most of proteins in a single cell. Here we introduce a high-throughput, multiplexed nanosystem to profile single cell proteome, either secretome or cytoplasmic phosphoproteome (Figure 1). We show each chamber with 0.1 nano-liter encapsulates one cell, and count as low as 100 molecules per cell. 8-24 phosphoproteins or cytokine/chemokine in single cells are quantified. T cell secretome has been profiled using the nanosystem platform, and subsets of a healthy donor sample are identified. We also demonstrate to use the nanosystem to investigate PI3K signaling pathway and identify signal flux in GBM cell lines. We find P-ERK pathway and P-Akt1 pathway coordinately promote proliferation of U87 EGFR VIII cells, which may explain high malignancy of GBM cancer with EGFR VIII expression.

Biography

Dr. Jun Wang joint NCI Alliance - Nanosystems Biology Cancer Center at California Institute of Technology as a postdoctoral fellow upon completion of his Ph.D in 2010 from Purdue University. He is also a research staff in UCLA School of Medicine. He has published more than 20 peer reviewed journal papers, with most of them at the interface of nano/micro technology and proteomics. He is also an active referee for journals such as Chemical Communications, Journal of Materials Chemistry.