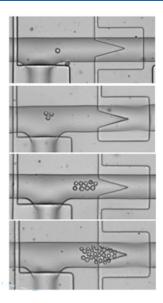
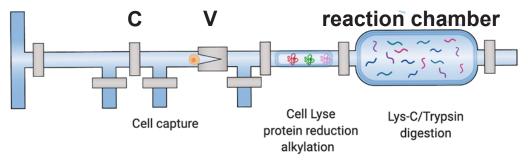
ETH zürich

Licensing Opportunity

Microfluidic device for quantitative single cell proteomics





(above) Capturing process in a microfluidic chip: Valve C and V control the flow of the suspending medium in the trapping region. While the suspending medium can pass the leaky V-valve, cells are retained. By adjusting the flow, the number of trapped cells is set. Once the cell(s) have been isolated, the processing (lysing and decomposition) and analysis by mass spectrometry follows in subsequent units. (left) Microfluidic device separating a controlled number of cells for analysis.

Application

This microfluidic device is capable of trapping single cells and performing sample preparation for proteomic analysis. The combination of multiple units enables the processes of cell injection, capture, lysis and detection to be completed on a single microfluidic device. A variety of such different multistep procedures may be run in parallel, an approach that drastically increases the throughput of the technique. This device can also bring multiple cells together for interaction and separates them afterwards, i.e. a T-cell and a cancer cell.

Features & Benefits

- precise and reproducible sample preparation for single cell analysis
- quantification of > 1'000 proteins within a single cell
- minimizing sample volume (nanolitres)

Publications

• Patent pending, WO 2023274997



ETH transfer transfer@sl.ethz.ch www.ethz.ch/transfer Reference 2021-033

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Technology Readiness Level



Background

Proteomics advances our comprehension of diseases. The proteins produced by cells offer insights into potential molecular targets for drugs and serve as molecular markers for the early diagnosis of diseases. A key challenge in proteomics is accurately quantifying protein copy numbers at the individual cell level. Each individual cell holds unique information and, thus the analysis of heterogeneous cell populations in bulk provides only averaged data about the multiple cells. Due to the cellular heterogeneity, the proteome information of every cell may be significantly different, and many low abundance information may be lost in the background. To truly delve into the intricacies of diseases and cellular behavior, a precise single-cell protein analysis is needed.

Invention

The small sample volumes for single cell analysis are handled by a microfluidic device with the ability to capture a controlled number of cells - down to a single cell. This microfluidic device incorporates a specialized trapping region containing a set of valves, including a unique valve known as the V-valve. As the suspending medium flows through the device, the leaky V-valve retains the targeted cell within the trapping region. Once the cell is successfully isolated, the leaky valve opens, allowing the cell to progress to the next chamber. In this chamber, the cell is lysed, and the extracted proteins are then transferred to another reaction chamber for digestion. Finally, the decomposed proteins are subjected to analysis using mass spectrometry techniques. This innovative approach not only addresses the challenges of working with minuscule sample volumes but also enables detailed and precise examination of individual cells.