New project

# Microchamber arrays for Observation and Characterization of in vitro Translation


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## Context

Protein microarrays allow the high-throughput analysis of target-protein-small-molecule interactions [1]. The binding profile of a small organic molecule for an entire proteome can be obtained in a few days. To this end, the proteins to be analyzed are purified and immobilized on a surface such as a glass microscope slide. Several problems exist with protein chips such as the amount of crude protein extract required and protein stability. Cell-free protein synthesis uses the translation machinery and metabolic enzymes naturally present within a cell to perform protein synthesis in vitro. It is widely used for protein production [2]. Efficient protein synthesis in microchambers would be an advantage to allow the production of arrays of proteins of interests "in situ" that can be use for protein chip development. Such microchamber arrays may also be used for an in vitro protein selection/evolution scheme. On a more fundamental aspect, it would also allow the direct study of the dynamics of protein synthesis even at a single molecule level.

## Objectives

We propose to perform efficient in vitro protein synthesis in microchamber arrays either using an in vitro translation system or directly from the condense material of a cell (molecular crowding conditions).

## Methods

We will design microfluidic systems in order to perform highly efficient protein synthesis in microchamber arrays. The systems will also include the trapping of single cells in microchambers and membrane disruption in order to use the cell material for protein synthesis.

## References and Publications


[1] G. C. Terstappen, C. Schlüpen, R. Raggiaschi and G. Gaviraghi, Nature Reviews. Drug. Discovery., 6, p.891, 2007

[2] T. Kigawa and S. Yokoyama, J. Biochem (Tokyo), 110, p.166, 1991.